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Title:
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Listing first 45 summaries
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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 BLOSUM62
Gapop 10.0 ,
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2024
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Copyright (c) 1993 - 2006
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RESULT 1
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ALIGNMENTS

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Best Local Simi
Matches 390;
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01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
12-OCT-1999;
12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes transmembrane receptors, preferably human grotein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AABA981285 represent sequences used in the
              02-NOV-2000
                                      AAY71297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-endogenous, human G protein-coupled receptors for scrinverse or partial agonists useful as therapeutic agents.
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                                                                                                                                           CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                                                                                                                                             LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
                                                                                                                                                                                                                                                STEVPAS FHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARR
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                                                                 standard;
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iaw CW, Lin I, I
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              (first entry
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99US-0157293P.
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99US-00416760.
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Pred. No. 1.5e-211;
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Query Match Best Local Sim Matches 390;

Similarity

100.0%; Score 2024; DB 3; 100.0%; Pred. No. 1.5e-211; tive 0; Mismatches 0;

Length Indels

0

390;

Conservative

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The present amino acid sequence is the hRUP7, an endogenous human orphan CC G protein-coupled receptor (GPCR). The full length hRUP7 CDNA was cloned CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan CC GPCR of the invention, like all GPCRs has seven transmembrane alpha CC helices with an extracellular N-terminus and an intracellular C-terminus. CC However, no endogenous ligands has yet been identified for the proteins CC of the invention. The orphan GPCRs may be used in the identification of CC their endogenous ligands, and to screen potential GPCR agonists and CC used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid CC encoding human orphan GPCRs may be used for tissue localisation CC expression analysis to provide information about their function in CC healthy and pathological states
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
                                                                                                                                                                                                                                                   Novel human orphan G protein-coupled receptors and the encoding cDNAs use in the identification of G protein-coupled receptor agonists.
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29-JUN-1999;
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28-MAY-1999;
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transmembrane receptor; signal cascade.
Sequence 390
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                   This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of PFI-013 are useful in the manufacture of a medicament for treating allergic disorder, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstitial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
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                                                                                                                                                                                                                                                               New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with sig transduction e.g. allergic, inflammatory, pulmonary, neoplastic dis-
                                                                                                                                                                                                                  Claim 22;
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20-APR-2000; 2000GB-00009973.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                       histamine H3 receptor homologue; infection; viral; bacterial; funga protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris;
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                                                                                                                                              G protein-coupled receptor; 7TM receptor;
                                                                                                                                                                                                                                                                                                                                                                             protein;
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     stroke; ulcer; migraine; vomiting;
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Pred. No. 1.5e-211;
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                                                                                                                      bacterial; fungal;
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cc and variants. Like all G protein-coupled receptors, AUGN35 liagnelles compression vectors and is involved in signal transduction. AVGR35 has for putative transmembrane domains and is involved in signal transduction. AVGR35 has compression of AVGR35 has for putative expression vectors and host cells comprising AXGR35 has for expression of AXGR35, and to an AXGR35 specific antibody. AXGR35 proteins compression axGR35, and to an AXGR35 specific antibody. AXGR35 proteins compression of AXGR35, and to an AXGR35 specific antibody. AXGR35 proteins compression axGR35 proteins compression axGR35 proteins compression of AXGR35 proteins compression and collections and to an AXGR35 specific antibody. AXGR35 proteins compression and collections particularly compression accurately compression and collections; pain, cancers, benign prostatic hypertrophy; compression accurately compression, and proteons; asthma; asthma; allergies; compression; accurate heart failure; hypotension; hypertension; angina compression, depression, stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, compression, and depression, delirium, dementia, and severe mental compression; and dyskinesias, such as parkinson's disease, Huntington's compression and compression and axGR35 proteins and compression axGR35 proteins ax
asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosing or determining susceptibility of an individual to disease via the detection of abnormal levels of protein or mRNA, or via the detection of mutations in the corresponding gene. AXOR35 proteins at also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nucleotides are also useful as diagnostic reagents, in chromosome localisation and tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delirium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; diles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
                                                   expression studies, and for producing transgenic animals useful in discovery. AXOR35-specific antibodies are useful for purifying the protein or fragments thereof, and are also useful for treating concassociated with the expression of the AXOR35 protein. The present sequence represents human AXOR35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-NOV-1999; 99US-00431898
03-FEB-2000; 2000US-00497790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 50-51; 54pp; English.
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D, Morrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor; signal transduction; mental disorder; central nervous system disease; metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder; psychotic disease; infection; HIV-1; HIV-2; pain; neurological disorder; psychotic disorder; Huntington's disease; schizophrenia; migraine; depression; anxiety; bipolar disorder; dementia; Alzheimer's disease; parkinson's disease; proliferative disorder; cancer; psoriasis; benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia; thyroid disorder; cardiovascular disease; hypotension; hypertension; thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis; inflammatory conditions; autoimmune disorder; rheumatoid arthritis; hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic; antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant; antiatherosclerotic; neurologytic; antimigraine;
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anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;
antipsoriatic; gene therapy; receptor.
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                                                                                                                                                                                                                                                                     /label= Transmembrane_domain_l
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                               /label= Transmembrane_domain_3
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                            Transmembrane_domain_5
                                                                                  Transmembrane_domain_4
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DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120

DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV

120

61

MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS

60

60

MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS

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CC 2067, to antibodies specific for nGPCR-2067, to drug screening methods

CC that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067

CC nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants

CC and species homologues and may also be used in genetic mapping. The

CC invention also discloses the use of nGPCR-2067 nucleic acids in screening

CC for a predisposition to nGPCR-2067-associated hereditary mental

CC disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic

CC acids may additionally be used to generate transgenic animals, including

CC knockout animals, which may provide an insight into treating a variety of

CC molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,

CC and nGPCR-2067 modulators may be used to treat a wide variety of medical

CC conditions, particularly mental disorders, central nervous system

CC diseases, and metabolic diseases. Diseases that may be treated include

CC viral infections, particularly HIV-1 or HIV-2 infections; pain; central

CC disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,

CC disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,

CC disease, such as cancers, benign prostatic hypertrophy and psortiasis;

CC metabolic disorders such as diabetes, dyslipidaemia, obesity, and

CC mypertension, thromosels, inflammatory conditions; autoimmune disorders (e.g.,

rheumatoid arthritis); hormonal disorders, and renal failure
                 Query Match
Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel human G protein-coupled receptor (GPCI designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative transmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-2061 acids encoding nGPCR-2067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                             Sequence 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encodes the novel protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).
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                   Local Similarity
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)B; ABA02496.
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Conservative
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                 100.0%; Score 2024; DB 5; 100.0%; Pred. No. 1.5e-211;
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                  chromatography, in immunoassay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
                                                                                                                                                                                                                                                             This sequence represents the amino acid sequence of a human histamir receptor (HR) designated SP9144. The sequence was isolated by search databases with the sequence of known G-coupled protein receptor (GCI The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; histamine receptor; chromosome 18; anti-inflammatory; anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke; anti-migratine; cardiant; anti-rheumatic; anti-arthritic; antipsoriatic; neuroprotective; inflammation; asthma; allergy; atopic dermatitis; myocardial infarction; migraine; chronic obstructive pulmonary disease; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding antigenic part of human histamine receptor, useful for preparing antibodies, e.g. for treating-histamine related
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DB; ABZ80663.
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                                                                                              BEHAN J X.
HEDRICK J A.
LAZ T M.
MONSMA F J.
MONSE K L.
UMLAND S P.
WANG S.
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Best Local S
Matches 390
                                                                                    Histamine H4 reception antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                      AAMS0564 standard;
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N-PSDB;
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Best Local Similarity
Matches 390; Conserv
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the proteins, useful in gene therapy for treating diseases where
beneficial to elevate mammalian histamine H4 receptor activity.
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 CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                   CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                                                    LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
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                 The invention provides an isolated histamine receptor, H4, which binds CC ligands comprising inidazole attached to amine by an alkyl chain. The H4 CC receptor can be expressed by standard recombinant methodology. Cells CC expressing H4 receptor protein at a detectable level can suppress cyclic can denosine monophosphate (cAMP) formation when contacted with the H4 CC receptor agonist. The H4 receptor and antibodies are used for identifying CC H4 receptor modulators. Modulation of histamine H4 receptors is useful CC for treating transplanted organ rejection, asthma, allergies and CC autoimmnue pathologies such as multiple sclerosis, type I diabetes, CC rheumatoid arthritis, cognitive and memory defects. The h4 receptor protein and nucleic acids are useful targets to identify drugs that are CC processes. Identification and isolation of H4 receptor provides for CC development of screening of molecules that interact with H4 receptors. CC Genetic variants of H4 can be used to diagnose an H4 associated disease as described above. The H4 receptor polymucleotide is useful to treat or prevent a disorder associated with the function of H4 in peripheral blood of lateract with the peripheral blood contents of the harmony hears and a looker associated with the function of H4 in peripheral
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13-NOV-2000; 2000US-0247855P.
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sclerosis and rheumatoid arthritis.
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The present sequence represents
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                                                                                                                                                                                                                                                                      23-JUN-2000; 2000US-0213461P
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                                                                                               2002-147880/19.
DB; ABK12959.
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                                                                                                                                                                                                                     TULARIK INC.
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                                                                                                                                                                    Zhao J,
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ilarity 100.0%;
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                                                                                                                                                                         Cutler
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Pred. No. 1.5e-211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390
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New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dysiexia and cardiac myxoma.

26; Page 61; 78pp; English.

CC The present invention relates to a new G-protein coupled receptor (GPCR)
CC polypeptide comprising greater than 70% amino acid sequence identity to
CC the amino acid sequence of human GPCRs TGR62, TGR213.1, TGR130.2,
CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or
CC 90% amino acid sequence identity to human novel edg receptor protein, as
CC defined in the specification. The GPCR covalently linked to a solid phase
CC is useful for identifying a compound that modulates signal transduction.
CC The identified compounds are useful for treating kidney disease, cerebral
CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac
CC myxoma. The molecules of the invention are useful for disgnosing
CC disorders or conditions such as kidney-related conditions or diseases
CC urinary abnormalities, renal tubule defects, hypertension and
CC urinary abnormalities, renal tubule defects, hypertension and
CC infiltrations, lesions, functional disease or condition e.g. cirrhosis,
CC infiltrations, lesions, functional disorders and jaundice and spleenCC associated disorders or conditions e.g. splenic enlargement, immune
CC disorders, blood disorders and others. Modulation of the polypeptide of
CC the invention is useful to treat or prevent any of the above conditions
CC or diseases. The present amino acid sequence represents the human GPCR
CC TGR62 protein of the invention. This sequence is one of seven novel G
CC protein coupled receptors of the invention (AAU74904-AAU74911)

Sequence 390 Ŗ,

맑 Ş S 밁 S 밁 Ś 밁 S S 밁 밁 Ś Query Match Best Local Sim: Matches 390; 361 361 301 301 241 241 181 121 181 121 61 61 ب Similarity LAKSLAILLGVEAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL LEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS STEVPASFHSERQRRKSSLMFSSRTKMNSNTTASKMGSFSQSDSVALHQREHVELLRARR STEVPASFHSERORRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARR DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS SYRTOHTGYLKIVTLMVAVWYLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS LEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA Conservative 100.0%; 0 Score 2024; DB 5; Pred. No. 1.5e-211;); Mismatches 0; 390 390 Length 390; Indels 0, Gaps 360 300 300 240 180 180 120 120 60

ABG711960
ID ABG711960
ID ABG711
XX ABG71
XX ABG71
XX 28-JA
XX 28-JA
XX XX XX Human
XX Human
KW macro
KW gastr

ABG71960 standard; protein; 390 8

ABG71960

(first entry)

Human G-protein coupled receptor AXOR35.

Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte; macrophage; eosinophil; neutrophil; infection; transplant reject gastrointestinal disorder; gastric ulcer; inflammatory bowel dis

Crohn's disease; irritable bowel syndrome; vomiting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; renal ischaemia; arteriosclerosis; atherosclerosis; psychosis; neurological disorder; migraine; anorexia; anxiety; schizophrenia; dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock; are the first and the sease; cancer; obesity; stroke; septic shock; versus host disease; osteoporosis.

US2002137054-A1

26-SEP-2002

20-JUL-2001; 2001US-00910411

02-NOV-1999; 99US-00431898 03-FEB-2000; 2000US-00497790 20-OCT-2000; 2000US-00693761

(SMIK) SMITHKLINE BEECHAM CORF

Aubart KM, Bergsma DJ, F: Michalovich D, Morrow DM, Fitzgerald L, Graybill 1

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2003-074982/07. DB; ABS57063.

Novel isolated G-protein coupled receptor polypeptide, AXOR: treating infections, gastrointestinal disorders, autoimmune urological diseases, cardiovascular diseases and cancer. AXOR35, disorders, useful for

Claim 1; Page 22; 24pp; English

The invention relates to an isolated G-protein coupled receptor CC polypeptide, AXOR35, (and its homologues and variants) and its encoding CC polynucleotide (and its homologues, variants, complements and RNA CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 (expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of CC vector into a cell such that the host cell produces AXOR35, a membrane of CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agnists or antagonists or antagonist or antagonist identified is useful for treating a disease such as asthmat, or for inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agnists or antagonists. The CC agonist or antagonist or neutrophils in diseased tissue such as sthmatic lung. AXOR35 or polymucleotide is useful in diagnostic assays, cc for identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or CC viral infections), transplant rejection, gastrointestinal disorders (such as gastribed bowel syndrome, vomiting, inflammation (such as Trohn's disease), critiable bowel syndrome, vomiting, inflammation (such as acopic cardiovascular diseases (such as urinary retention), pypotension, CC disease), cough, renal diseases (such as urinary retention), pypotension, cc disease), cancexia, anxiety, schropic obstructive pulmonary disease), cancer, obesity, stroke, septic shock, graft cresus host disease and osteoporosis. The present sequence represents

390

Query Match Best Local S Matches 390 Local Similarity tes 390; Conser 100.0%; Score 2024; ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches 1.5e-211; В 6 Length 390; <u>,</u> Gaps

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RESULT 13
ABU92265
ID ABU92265
AC ABU92
XX ABU92
XX Human
XX Human
XX Human
XX Homo
XX Homo
XX US200
XX 16-FE
PR 12-FE
PR 16-FE
PR 12-M
PR 18-M
PR 28-M
PR 29-SI
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28 MAY 1999
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                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1998;
16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA
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                     I O H P
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990S-0123944P
990S-0123943P
990S-0136436P
990S-0136437P
990S-0136567P
990S-0137127P
990S-0137121P
990S-0141448P
990S-01566333P
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99US-0120416P
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RESULT 14
ABP81727
ID ABP81
XX ABP81
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XX O4-MA
DT 04-MA
XX Human
XX Human
XX G pro

standard;

protein;

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Human 04-MAR-2003 ABP81727; ABP81727

histamine

H4 receptor

protein SEQ ID NO:629

(first

entry

protein-coupled receptor; GPCR; antigenic peptide;

gene therapy;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a human G protein-coupled receptor (GPCR) cappearing as AU992259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP5, hRUP5, hRUP7, hGPCRZ7, hARE-1, hARE CC -2, hppR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN9 and hRUP4. CC Also included are a plasmid comprising a vector and one of the cDNAs CC above and a host cell comprising the plasmid. The GPCRS are useful for CC the direct identification of candidate compounds as inverse agonists, CC agonists or partial agonists. In vitro and in vivo systems incorporating CC GPCRs is useful for elucidating and understanding the roles these CC receptors play in the human condition, both normal and diseased, as well CC as understanding the signalling cascade. The cDNAs are useful for making a CC understanding the signalling cascade. The cDNAs are useful for making a CC identification of the expression of the receptor in tissue samples. The CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR CC identification of the expression of the receptor in tissue samples. The
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Best Local S
Matches 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R,
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                                                                                                                                                                                                                                                                                                                                   43
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                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                          CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                                                       LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
                                                                                                                                                                                                                                                                                    SYRTOHTGYLKIYTLMVAVWYLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF 180
                                                                                                                                                                                                                                                                                                                                 390 AA;
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                                                                                                                                                                                                                  LEFVIPVILVAYFMMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA
                                                                                                                                  STEVPASFHSERORRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARR
                                                                                                                                                                STEVPASFHSERORRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARR
                                                                                                                                                                                                                                                                 SYRTQHTGVLKIVTLMVAVMVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF
CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                                                                                                                                                                  LEFVI PVILVAYFNMNI YWSLWKRDHLSRCQSHPGLTAVSSNI CGHSFRGRLSSRRSLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2024; DB 6; ilarity 100.0%; Pred. No. 1.5e-211; Conservative 0; Mismatches 0;
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g protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease, autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthms; tuberculosis; obesity; nausea; trauma.

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                                                                                                                                  The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABB82019) to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC aride. Also described: (1) an assay for the detection of a particular GC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC antibody against a particular GPCR, and in the production of specific presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs are useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CC treating immune-related diseases, growth-related diseases, cell CC effects and antibodies are also useful for describe for CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC atherosclerosis, bacterial, fungal, protozoan or viral infections. CC atherosclerosis, bacterial, fungal, protozoan or viral infections. CC disease, parkinson's disease, multiple sclerosis, pain, sporiasis, CC anxiety, depression, schizophrenia, dementia, mental retardation, memory CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, CC any other disorder in which GPCRs are involved. The antibodies may be CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ4253 encode CC GPCR proteins given in ABP81675 to ABP82018, which are used in the cCC exemplification of the present invention
                                                              Query Match
Best Local Simi
Matches 390;
                                                                                                                                Sequence 390 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypertension;
ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2000; 2000US-0257144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2001; 2001WO-US050107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w isolated antigenic peptides e.g., for G protein-coupled receptors PCR), useful for diagnosing and designing drugs for treating conditions which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or toimmune diseases.
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                                                                               Similarity
               MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 1; 523pp; English
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roush CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotension;
                                                                               100.0%;
   STRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
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                                                                 0,
                                                                               Score
Pred.
                                                                 Mismatches
                                                                            2024; DB 6;
No. 1.5e-211;
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                                                                                               Length
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis; trauma;
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DFPVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV

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                                                                             The invention relates to splice variants of human H4 histamine receptor H4b and H4C. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4C is useful for treating inflammation, asthma, allery, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                       Novel splice variants of human H4 histamine receptor, H4b and H4c, useful for identifying agonists or antagonists of the receptor which are useful for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                                                                                                                                         Example; Page 58-60; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallagher MJ,
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13-NOV-2001;
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)B; AAD55126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H4 receptor wild-type protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatitis; stroke; myocardial infarction; migraine; allergy; cobstructive pulmonary disease; COPD; cerebroprotective; therapy; cobstructive pulmonary disease; inflammation; neuroprotective; therapy;
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Search completed: March 28, 2006, 13:54:32 Job time : 190 Becs

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5.1.7 Biocceleration Ltd

alpha-1C-adrenergi

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(;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Accession: JC7566
C;Accession: JC7566
R;Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.
Biochem. Biophys. Res. Commun. 279, 615-620, 2000
A;Title: Molecular cloning and characterization of a new human h
A;Reference number: JC7566; MUID: 20568725; PMID:11118334
A;Cottents Leukocyte
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A;Gene: hh4r
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9H3N8; UNIPARC:UPI0000039A92; DDBJ:AB045370 C;Comment: This receptor, belonging to the biogenic amine receptors of G
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A; Residues: 1-390 <NAK>
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                 CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
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I39369
A53279
A47321
JH0170
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DYBOD2
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S10856
A31897
JC5042
JN0268
A35375
I57959
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alpha-1A-adrenergi
alpha-1A-adrenergi
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alpha-1C adrenergi
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protein-couple

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Gaps

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180

180

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240

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histamine receptor,

HH4R

09-Jul-2004

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muscarinic acetylcholine receptor M2, glandular - pig N;Alternate names: muscarinic acetylcholine receptor III C;Species: Sus scrofa domestica (domestic pig) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change C;Accession: S01114 R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P49578; UNIPARC:UPI00001252B4; C;Superfamily: vertebrate rhodopsin C;Keywords: neurorecarries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Gadbut, A.P.; Galper, J.B.
J. Biol. Chem. 269, 25823-25829, 1994
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed A;Reference number: A55019; MUID:95014393; PMID:7929287
A;Accession: A55019
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A; Residues: 1-639 < GAD>
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;Accession: S01114
;Akiba, I.; Kubo, T.; Maeda, A.;
EBS Lett. 235, 257-261, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uscarinic acetylcholine receptor, M3 isoform - chicken
;Species: Gallus gallus (chicken)
;Date: i1-Nov_1994 #sequence_revision 11-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A55019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSLACADLIIGVISMNLFTTYIIMGHWALGNLACDLWLSIDYVASNASVMNLLVISFDRY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNLAISDFFVGVISIPLYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                       KQQYQQRQS
                                                                                                                                                                                                                                                        LVNTFCDCV--PKTVW-NLGYWLCYINSTVNPVCYALCNKMFRNTFKMLLLCQCDKRKRR
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Pred. No. 2.2e-28;
2; Mismatches 151
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                      M.; Numa, S.
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A;Title: Primary structure of porcine muscarinic acetylcholine receptor III
A;Reference number: S01114; MUID:88296835; PMID:3402600
A;Accession: S01114
A;Molecule type: DNA
A;Residues: 1-590 <AKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;231-252/Domain: transmembrane #status F;493-513/Domain: transmembrane #status F;528-546/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;105-125/Domain: transmembrane #status predicted F;143-164/Domain: transmembrane #status predicted F;185-207/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter
F;68-91/Domain: transmembrane #status predicted <TM1>
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                               NPLLYPLCHKRFQKAFLKIF---CIKKQPLPSQHSRSVS 389
                                                                SLIKEKKAAQTLSAILLAFIITWTPYNIMVLVNTFCDSCI-PKTYW-NLGYWLCYINSTV
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                                                                                          ELLRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFV 353
                                                                                                                                                                                                                                                                RSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDIGSET
                                                                                                                                                                                                                                                                                                                                                                   VAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLS------
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NPVCYALCNKTFRTTFKMLLLCQCDKRKRRKQQYQQRQS
                                                                                                                              KSFSKLPIQLESAVDTAKASDVNSSVGKTTATLPLSFKEATLAKRFALKTRSQITKRKRM
                                                                                                                                                               QSDS----
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Pred. No. 5.4e-27;
8; Mismatches 151
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <LEE>
A;Cross-references: UNIPROT:P41984; UNIPARC:UPI00001252B3; EMBL:U08286; NID:g520465; PI
C;Superfamily: vertebrate rhodopsin
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muscarinic acetylcholine receptor m3 - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 C;Accession: 847572

#text_change

09-Jul-2004

RESULT 4 S47572

RiLee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J. Biochim. Biophys. Acta 1223, 151-154, 1994
A;Title: Cloning and expression of a CDNA encoding bovine A;Reference number: S47572; MUID:94339178; PMID:8061048

muscarinic acetylcholine

3

A; Reference number: A; Accession: S47572

422 246

479

246

203

222

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A;Residues: 1-590 <PER>
A;Cross-references: UNIPROT:P20309; UNIPARC:UPI0000050453; EMBL:X15266; NID:g32323; PIDN C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme rj68-95/Domain: transmembrane #status predicted <TM12>
F;105-131/Domain: transmembrane #status predicted <TM3>
F;143-164/Domain: transmembrane #status predicted <TM4>
F;143-207/Domain: transmembrane #status predicted <TM5>
F;193-513/Domain: transmembrane #status predicted <TM6>
F;493-513/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscarinic acetylcholine receptor M4 - human
C;Species: Homo sapiens (man)
C;Species: 1-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10128
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J
EMBO J. 6, 3923-3929, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S10128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expi
A;Reference number: S04326; MUID:88166632; PMID:3443095
A;Accession: S10128
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                                                              Query Match
Best Local S
Matches 118
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Best Local S
Matches 120
                                                                                                                                                                  15,41/Binding site: carbohydrate
                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120;
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                  VTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVISIPLYIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPVCYALCNKTFRNTFKMLLLCQCDKRKRRKQQYQQRQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSFSKLPIQLESAVDTAKASDVNSSVGKTTATLPLSFKEATLAKRFALKTRSQITKRKRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDIGSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMIGLAWVISFILWAPAILFWQYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYMPVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMVAV-WVLAFLVNGPMILVSESWKDEGS----ECEPGFFSEWYILAITSFLEFVIPVIL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGVLKIVT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTI----LYWRIYKETE-KRTKELAĞLQASGTEAEAENFVHPTGSSRSCSSYELQQQSMK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFIAFLTGVLALVTIIGNILVIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMNLFTTY 128
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                                                                   95;
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                                                              Score 411; DB
Pred. No. 1.2e
95; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 413; DB 2;
Pred. No. 7.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 160;
                                                                                                                                                                    (Asn)
                                                                                      411; DB 2;
No. 1.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SSRTKMNSNTIASKMGSFSQSD-----
                                                                                                                                                                    (covalent)
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                                                                                                                Length 590
                                                                   Indels
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                                                                                                                                                                  #status predicted
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                                                                   158;
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A;Residues: 104-100 (NPIARC:UPI00001778C3)
A;Cross-references: UNIPARC:UPI00001778C3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter
F;67-90/Domain: transmembrane #status predicted <TM1>
F;104-124/Domain: transmembrane #status predicted <TM2>
F:142-163/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                        A;Experimental source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequence
R;Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues involved a;Reference number: A37121; MUID:90337982; PMID:2380182
A;Accession: B37121
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-269;463-589 <BO2>
A;Cross-references: UNIPARC:UPI00001778C1; UNIPARC:UPI00001778C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Identification of a family of muscarinic acetylcholine receptor genes. A;Reference number: A94293; MUID:87263421; PMID:3037705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P08483; UNIPARC:UPI0000163B75 R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R. Science 237, 527-532, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscarinic acetylcholine receptor M3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989
C;Accession: B94518; B94293; B37121; B29514
                                                                                                                                                                    A; Molecule type: protein A; Residues: 104-166 < KUR>
                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: B94293
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A; Residues: 1-589 < BO1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to GenBank, July 1987 A; Reference number: A94518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSHPGLTAVSSN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TIASKMGSFSQSDSVALHQRE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RGRLSSRRSLSASTEVPA
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                                                                                                receptor;
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Best Local Similarity

23.3%;

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A AEXperimental source: brain

G:Superfamily: vertebrate rhodopsin

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme

F:67-90/Domain: transmembrane #status predicted <TM1>
F:104-124/Domain: transmembrane #status predicted <TM3>
F:142-163/Domain: transmembrane #status predicted <TM3>
F:142-163/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                    C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.;
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by A;Reference number: A29476; MUID:88077068; PMID:3120722
A;Accession: A29476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;184-206/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM7>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-589 < BRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVCYALCNKTFRTTFKTLLLCQCDKRKRRKQQYQQRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIKEKKAAQTLSAILLAFIITWTPYNIMVLVNTFCDSCI-PKTYW-NLGYWLCYINSTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYFNMNIYWSLWK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIMNRWALGNLACDLWLSIDYVASNASVMNLLVISFDRYFSITRPLTYRAKRTTKRRGVM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLLYPLCHKRFQKAFLKIF---CIKKQPLPSQHSRSVS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTKLPIQLESAVDTGKTS-DTNSSADKTTATLPLSFKEATLAKRFALKTRSQITKRKRMS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYSIVLKLPGHSSILNSTKLPSSDNLQVSNEDLGTVDVERNAHKLQAQKSMGDGDNCQKD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----FHSERQRRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDIGSETRA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TI----LYWRIYKETEKRTKELAGLQASGTEAEAENFVHPTGSSRSCSSYELQQQGVKRS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGVLKIVT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFIAFLTGFLALVTIIGNILVIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMNLFTTY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RDHLSRC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGLA-WVISFVLWAPAILFWQYFVGXXTVPPGECFIQFLSEPTITFGTAIAAFYMPVTIM 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                            transmembrane
                                                                 transmembrane
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  20.2%;
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                                            #status
                                                                     #status
  Score
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                                         predicted predicted
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408;
                                                                                      predicted
В
2;
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                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-307,'D',309-338,'K',340-484 <VA2>
A;Cross-references: UNIPARC:UPI0000130B66; EMBL:X69521; NID:g871406; PIDN:CAA49269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Neurochem. 64, 2387-2395, 1995
A;Title: Characterization of a cloned locust tyramine receptor A;Reference number: 858868; MUID:95279966; PMID:7780020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor GCR1 - migratory locust C;Species: Locusta migratoria (migratory locust) C;Species: Locusta migratoria (migratory locust) C;Date: 15-Feb-196 #sequence_revision 01-Mar-1996 #text_change C;Accession: S58868; S58869
R;Vanden Broeck, J.; Vulsteke, V.; Huybrechts, R.; De Loof, A.
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                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q25321; UNIPARC:UPI0000130B64; A;Accession: S58869
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Best Local
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                                        55 AVSLSLIILITIVGNVLVVLSVFTYKPLRIVQNFFIVSLAVADLTVAVLVMPFNVAYSLI
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPLLYPLCHKREQKAFLKIE---CIKKQPLPSQHSRSVS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFIAFLTGELALVTIIGNILVIVAFKVNKQLKTVNNYFLLSLACADLIIGVISNNLFTTY
E-WDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGVLKIVTLMV 137
                                                                                   AFFMSLVAFAIMLGNALVILAFVVDKNLKHRSSYFFLNLAISDFFVGVISIPLYIPHTLF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLIKEKKAAQTLSAILLAFIITWTPYNIMVLVNTFRDSCI-PKTYW-NLGYWLCYINSTV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSRRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDIGSETR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAYFNMNIYWSLWK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMIGLAWVISFVLWAPAILFWQYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYMPVTI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMVAV-WVLAFILVNGPMILVSESWKDEGS----ECEPGFFSEWYILAITSFLEFVIPVIL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGVLKIVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPVCYALCNKTFRTTFKMLLLCQCDKRKRRKQQYQQRQS 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIYSIVLKLPGHSSILNSTKLPSSDNLQVSNEDLGTVDVERNAHKLQAQKSMGDGDNCQK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RDHLSRC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTI----LYWRIYKETEKRTKELAGLQASGTEAEAENFVHPTGSSRSCSSYELQQQGVKR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELLRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFTKLPIQLESAVDTGKTS-DTNSSADKTTATLPLSFKEATLAKRFALKTRSQITKRKRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FHSERORRK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                 Conservative
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                                                                                                                              20.1%; Score 406.5; DB 2; 24.2%; Pred. No. 2.2e-26; Live 94; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89;
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9; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSHPGLTAVSSNICGHSFRGRLSS------
                                                                                                                                   Indels
                                                                                                                                                                         Length
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                                                                                                                                                                         484;
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alpha-1-adrenergic receptor - golden hamster

()Species: Mesocricetus auratus (golden hamster)

()Date: 22-Uan-1993 #sequence_revision 22-Uan-1993 #text_change 09-Uul-2004

()Accession: A40491

R;Cotecchia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz; R.J.; Caron, M.G.; Kobilka, B.

Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988

A;Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic A;Reference number: A40491; MUID:89017157; PMID:2845398

A;Accession: A40491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-515 <COT>
A;Residues: 1-515 <COT>
A;Cross-references: UNIPROT:P18841; UNIPARC:UPI0000124FC9; GB:J04084; NID:g619407; C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                        209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FFVGVISIPLYIP-HTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 SNSTLPQLDVTRAISVGLVLGAFILFAI-VGNILVILSVACNRHLRTPTNYFIVNLAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TNSTI-NLSLSTRVTLAFFM-SLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                   SYRTQHTGVLKIVTLMVAVWVLAFLVN-GPMILVSESWKDEGSECEPGFFSEWYILAITS
                                                                                                                                      MSNSKELTLRIHSKNFHEDT--LSSTKAKGHNPRSSIAVKLFKFS
                                                                                                                                                                                              LSASTEVPASFHSERQRRKSSLMFSSRTKMNS--NTIASKMGSFSQSDSVALHQREHVEL
                                                                                                                                                                                                                                                                                                          FLEFVIP--VILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRS
                                                                                                                                                                                                                                                                                                                                                                 QYPTLVTR-RKAILALLSVWVLSTVISIGPLLGWKEPAPNDDKEC--GVTEEPFYALFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGVRYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIYWS----LWKRDHLSRCQS----HPGLTAVSSNICGHSFRGRLSSRRSLSASTE----
                                                                              LRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIFNLDFRRAFKKLLHFK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLCHKRFQKAFLKIFCIK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYTCTTTTTTTTTAVTDSPRSRTASQKGSTAPPTPVQPKSIPVYQFIEEKQRISLSKE 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIFIATKRELRERAKASKLINSAMKQQMAAQAVPSSVPSH------DQESVSSETNHNEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVWLLSGVISSPPLIGWNDWPMEFNDTTPCQLTEEQGYVI-YSSLGSFFIPLFIMTIVYV 232
                                -REKKAAKTLGIVVGMFILCWLPFFIALPLGSLFSTLKPPDAV-FKVVFWLGYFNSCLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRAARTLGIIMGVFVVCWLPFFLMYVIVPFCNPSCKPSPKLVNFITWLGYINSALNPIIY 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FSSRTKMNSNT------IASKMGSFS----QSDSVALHQ----REHVELLRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 402.5; DB 2
Pred. No. 5.1e-26;
                                                                                                                                                                                                                                                        CRVYIVAKRITKNL-
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                                345
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                    , B
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;39-72/Domain: transmembrane #status predicted <TMi>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;81-111/Domain: transmembrane #status predicted <TM3>F;121-146/Domain: transmembrane #status predicted <TM3>F;157-184/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-158,'P',160-244,'H',246-314,'F',316-380,382-517 <WEI>A;Cross-references: UNIPARC:UPI00001778AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D. Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A; Title: Cloning, expression and characterization of human alpha adrenergic receptors A; Reference number: JC2331; MUID:94296402; PMID:8024574
A; Accession: JC2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:ADRA1B
A;Cross-references: GDB:127901; OMIM:104220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P35368; UNIPARC:UPI0000149ED4; GB:M99590; NID:g178211
A;Note: sequence extracted from NCBI backbone (NCBIP:116785)
A;Note: this translation is not annotated in GenBank entry HUMADRENB, release 113.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-517 < RAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ramarao, C.S.; Denker, J.M.; Perez, D.M.; Galvin, R.J.; Riek, J. Biol. Chem. 267, 21936-21945, 1992
A;Title: Genomic organization and expression of the human alpha A;Reference number: A45121; MUID:93016158; PMID:1328250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A45121; JC2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-1B adrenergic receptor -
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              152 QYPTLVTR-RKAILALLSVWVLSTVISIGPLLGWKEPAPNDDKEC--GVTEEPFYALFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 LLYPLCHKRFQKAFLKI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TNSTI-NLSLSTRVTLAFFM-SLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISD
LLYPLCHKRFQKAFLKI 372
                                                                                                                                                                                                                     LSASTEVPASFHSERORRKSSLMFSSRTKMNS--NTIASKMGSFSQSDSVALHQREHVEL
                                                                                                                                                                                                                                                                                                                                    FLEFVIP--VILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNSTLPQLDITRAISVGLVLGAFILFAI-VGNILVILSVACNRHLRTPTNYFIVNLAMAD
                                                       -REKKAAKTLGIVVGMFILCWLPFFIALPLGSLPSTLKPPDAV-FKVVFWLGYFNSCLNP
                                                                                                         LRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNP 355
                                                                                                                                                                MSNSKELTLRIHSKNFHEDT--LSSTKAKGHNPRSSIAVKLFKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                SYRTOHTGVLKIVTLMVAVWVLAFLVN-GPMILVSESWKDEGSECEPGFFSEWYILAITS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLSFTVLPFSAALBVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGVRYSL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFVGVISIPLYIP-HTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.7%; Score 399.5; DB 2; 28.1%; Pred. No. 9.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1B-adrenergic
                                                                                                                                                                                                                              295
                                                             345
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alpha-1B-adrenergic receptor - rat C; Species: Rattus norvegicus (Norway rat) C;Date: 03-May-1994 #sequence_revision 03-May C;Accession: JC1525; S08400 R;Gao, B.; Kunos, G. Gene 131, 243-247, 1993 A;Title: Isolation and characterization of th A;Reference number: JC1525; MUID:94010315; PM A;Accession: JC1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
JC1525
A;Residues: 1-515 <GAO>
A;Residues: 1-515 <GAO>
A;Cross-references: UNIPROT:P15823; UNIPARC:UPI0000170842; GB:L08610; NID:g202624; PIDN R;Voigt, M.; K:appert, J.; Chin, H.
Nucleic Acids Res. 18, 1053, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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C;Superfamily: octopamine receptor type I
C;Keywords: disulfide bond; neurotransmitter receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 184, 245-250, 1997
A;Title: Molecular cloning of a putative serotonin receptor A;Reference number: JC6178; MUID:97183669; PMID:9031635
A;Accession: JC6178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                          A; Molecule type: DNA
                                                                                                                                                           A;Status: translation not shown
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A; Residues: 1-379 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Kawahara, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serotonin receptor - Barnacle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAVADLTVALFVLPLNVAYRLLNQWLLGSYLCQMWLTCDILCCTSSILNLCVIALDRYWA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAISDFFVGVISIPLYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELNASAAPLDDERELGETVAATALLLAIILVTIVGNSLVIISVFTYRPLRSVQNFFVVS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIYPCSSKEFKRAFVRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEVNPLLYPLCHKREQKAFLKI 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP--LAELESVASQEDETEPSPEPEPLSSRADKPAN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRSLSASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQ----R 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVYSSSGSFFIPLIIMSVVYAKIFFATKRR--LRERTRKLGTLAVPAP-----PQRTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI-TSFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITDPINYAQKRT-IRRVNTMIAAVWALSLVISVPPLLGWNDWPAQFTEDTPCTLTQERLF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDTNSTI-----NLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoai,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.4%;
25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 393.5; DB 2; Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371
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                                                                                                                                                                                                                                                                                                                                                                             03-May-1994 #text_change
                                                                                                                                                                                                                        the gene encoding PMID:8406017
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                                                                                                                                                                                                                                                         rat alpha 1B
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A;Accession: S08400
A;Molecule type: mRNA
A;Residues: 1-202,'C';
                                                                                                           F;444-464/Domain: transmembrane #status F;479-498/Domain: transmembrane #status
                                                                                                                                  F;105-126/Domain: transmembrane #status predicted <TM3>
F;147-169/Domain: transmembrane #status predicted <TM4>
F;192-214/Domain: transmembrane #status predicted <TM5>
F;192-214/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                    F;67-87/Domain: transmembrane #status predicted <TM1>F;67-87/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                             C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; glycoprotein;
                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-532 <BON>
A;Cross-references: UNIPARC:UPI00001778C4
                                                                                                                                                                                                                                                                                                                                                                                                           Neuron 1, 403-410, 1988
A;Title: Cloning and expression of the human and rat m5
A;Reference number: JT0530; MUID:90166521; PMID:3272174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Accession: JT0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-202,'C',204-206,'C',208-305,'C',307-414,'QK',417-439,'C',441-483,'ATA',48:
A;Cross-references: UNIPARC:UPI0000154B78; EMBL:X51585; NID:955557; PIDN:CAA35934.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor. A;Reference number: S08400; MUID:90192094; PMID:2156222
                                                                                      F;8,13/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JT0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Bonner, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         muscarinic acetylcholine receptor M5 -
                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                      Comment: Muscarinic acetylcholine receptors mediate many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: vertebrate rhodopsin;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J. 403-410, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245
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  Similarity 22.
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNSTI-NLSLSTRVTLAFFM-SLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIYPCSSKEFKRAFMRI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLYPLCHKRFQKAFLKI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSASTEVPASFHSERQRRKSSLMFSSRTKMNS--NTIASKMGSFSQSDSVALHQREHVEL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSFYIPLAVILVMY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLEFVIP--VILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNSTLPQLDVTRAISVGLVLGAFILFAI-VGNILVILSVACNRHLRTPTNYFIVNLAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSNSKELTLRIHSKNFHEDT--LSSTKAKGHNPRSSIAVKLFKFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYPTLVTR-RKAILALLSVWVLSTVISIGPLLGWKEPAPNDDKEC--GVTEEPFYALFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFVGVISIPLYIP-HTLPEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -REKKAAKTLGIVVGMFILSWLPFFIALPLGSLFSTLKPPDAV-FKVVFWLGYFNSCLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                      19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.4%; Score 392.5; DB 2
28.1%; Pred. No. 3.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
    , e
Score 392.5; DB 2;
Pred. No. 3.7e-25;
9; Mismatches 156;
                                                                                         (Agn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                             predicted
                                                                                           (covalent)
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                                                                                           #status
                                                                                                                                                                                                                                                                  neurotransmitter
                                             Length 532;
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      Indels 131;
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                                                                                           predicted
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      Gaps
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      14;
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R;Lai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske Adv. Exp. Med. Biol. 287, 313-330, 1991
A;Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy A;Reference number: I51837; MUID:92101806; PMID:1759615
A;Accession: I51837
                                                                                                                                                                                                                                                               A;Gene: m1
C;Superfam
                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-460 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscarinic receptor - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
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Best Local Similarity
                                                                                                                                                                                                                                                               Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 LMVAV-WVLAFLVNGPMILVSESWKDEGS----ECEPGFFSEWYILAITSFLEFVIPVIL 189
                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
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                                                                                                                              N
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                                                                YFILLSLACADLIIGTFSMNLYTTYLLMGHWALGTLACDLWLALDYVASNASVMNLLLISF 121
                                                                                             YFFLNLAISDFFVGVISIPLYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISY 110
                                                                                                                              NTSVPPAVSPNITVLAPGKGPWQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMLLLC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSNICGHSFRGRLSSRRSLSASTE------VPASFHSERORRKSSLMFSSRTKMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTILYCRIYRETEKRTKDLADLQGSDSVTKAEKRKPAHRALFRSCLRCPRPTLAQRERNQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAYFUMNIY----
DRYFSVTRPLSYRAKRTP--RRAALMIGLAWLVSFVLWAPAILFWQYLVGERTVLAGQCY 179
                                                                                                                                                            NSTINLSLSTRVT-----LAFF---MSLVAFAIMLGNALVILAFVVDKNLRHRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LKIFC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAFIITWTPYNIMVLVSTFCDKCV-PVTLWH-LGYWLCYVNSTVNPICYALCNRTFRKTF 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNQETNNGCHKVKIMPCPFPVÄKEPSTKGLNPNPSHQMTKRKRVVLVKERKAÄQTLSAIL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKESPGEEFSAEETEETFVKAETEKSDYDTPNYLLSPAAAHRPKSQKCVAYKFRLVVKAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILMGRWALGSLACDLWLALDYVASNASVMNLLVISFDRYFSITRPLTYRAKRTP--KRAG
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                                                                                                                                                                                              Conservative
                                                                                                                                                                                                              19.3%; Score 391.5; DB 2
25.8%; Pred. No. 3.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----W-KRDHLSRCQSHPG------LTAV 219
                                                                                                                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TIASKMGS--FSQSDSVALHQREHVELLRARRLAKSLAILL 309
                                                                                                                                                                                              Mismatches 149;
                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                              Indels 115;
                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                               460;
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                                                                                                                                                                                              Gaps
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F;142-168/Domain: transmembrane #status predicted <TM4>
F;167-209/Domain: transmembrane #status predicted <TM5>
F;367-387/Domain: transmembrane #status predicted <TM6>
F;402-420/Domain: transmembrane #status predicted <TM7>
F;2,12/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosph P;25-50/Domain: transmembrane #status predicted <TM1>F;62-93/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-27;338-460 <BO2>
A;Residues: 1-27;338-460 <BO2>
A;Residues: 1-27;338-460 <BO2>
A;Cross-references: UNIPARC:UPI00001778CE; UNIPARC:UPI00001778CF
A;Experimental source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequenc
A;Note: only a part of the protein translation is given; none of the nucleotide sequenc
A;Note: only a part of the protein translation is given; none of the nucleotide sequenc
A;Note: only a part of the protein translation is given; none of the nucleotide sequenc
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A;Reference number: A94518
A;Accession: A94518
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989
C;Accession: A94518; A94293; A37121; A29514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI00001778D0
C;Superfamily: vertebrate rhodopsin
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R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
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A; Residues: 62-124 < KUR>
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           52
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
           YFFLNLAISDFFVGVISIPLYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISY 110
                                                                                                               NTSVPPAVSPNITVLAPGKGPWQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNN
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                                                                                                                                                                                                                              NSTINLSLSTRVT-----LAFF---MSLVAFAIMLGNALVILAFVVDKNLRHRSS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIAFWLQWFNSFVNPLLYPLCHKRFQKAF-LKIFC-----IKKQP 379
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Pred. No. 3.8e-25;
4; Mismatches 149;
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401 ELGYWLCYVNSTVNPMCYALCNKAFRDTFRLLLLCRWDKRRWRKIPKRP 449	ДĎ
341 RIAFWLQWENSFYNPLLYPLCHKRFQKAF-LKIFCIKKQP 379	Ş
343 PRGKEQLAKRKTFSLVKEKKAARTLSAILLAFILTWTPYNIMVLVSTFCKDCV-PETLW- 400	ᅡ
287LHQREHVELLRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWY	Ş
286 ESLTSSEGEEPGSEVVIKMPMVDSEAQAPTKQPPKSSPNTVKRPTKKGRDRGGKGQK 342	В
260MFSSRTKMNSNTIASKMGSFSQSDSVA	8
236 GSSSSSERSQPGAEGSPESPPGRCCRCCRAPRILQAYSWKEEEEEDEGSM	ర్జ
219 VSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKSSL 259	Ş
180 IQFLSQPIITFGTAMAAFYLPVTVMCTLYWRIYRETENRARELAALQGSETFGKGG 235	멍
166 PGFFSEWYILAITSFLEFVIPVILVAYFNWNIYWSLWKRDHLSRCQSHPGLTA 218	Ś
122 DRYFSVTRPLSYRAKRTPRRAALMIGLAWLVSFVLWAPAILFWQYLVGERTVLAGQCY 179	망
111 DRYLSVSNAVSYRTQHTGVLKIVTLMVAV-WVLAFLVNGPMILVSESWKDEGSECE	8
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Search completed: March 28, 2006, 13:59:17 Job time: 42 secs

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Q91ZY2 MOUSE
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Q86SB1 MACMU
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Q540P3 MOUSE
Q54535 PHOSU
HRH3 CAVPO
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Q4g0i6 homo sapien
Q96ld9 homo sapien
Q8wnv9 sus scrofa
Q91zy1 rattus norv
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Q91zy2
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ALIGNMENTS

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Puhl H.L. III, Ikeda S.R., Aronstam R.S.;

"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: The H4 subclass of histamine receptors could mediate thistamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [6]
MUCLEOTIDE SEQUENCE.
MEDLINE=21106320; PubMed=11179436;
Michalovich D., Wu H.-L.,
Tierney L.A.,
                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
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                                                                                       PIR; JC7566; JC7566.
Ensembl; ENSG00000134489;
HGNC; HGNC:17383; HRH4.
MIM; 606792; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung, pancreas, skeletal muscle, prostate, small intestine, spleen, fetal liver and lymph node.

-!- INDUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

-!- MISCELLANBOUS: Does not bind diphenhydramine, loratadine, ranitidine, cimetidine and chlorpheniramine. Shows modest affinity for dimaprit, impromidine, clobenpropit, thioperamide, burimamide clozapine, immepip and imetit. The order of inhibitory activity was imetit > clobenpropit > burimamide > thioperamide.

Clobenpropit behaves as a partial agonist, dimaprit and impromidine show some agonist activity while clozapine behaves as a full agonist. Thioperamide shows inverse agonism (enhances cAMP activity). The order of inhibitory activity of histamine derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-methylhistamine > R(-)-alpha-methylhistamine behave as full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2001)
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"Identification of a histamine H4 receptor on human eosinophils in eosinophil chemotaxis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  absence of agonist).
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed primarily in the bone marrow an eosinophils. Shows preferential distribution in cells of immunological relevance such as T-cells, dendritic cells, monocytes, mast cells, neutrophils. Also expressed in a wide variety of peripheral tissues, including the heart, kidney, Tanorrass, skeletal muscle, prostate, small intestine,
GO:001621; C:integral to memb
GO:0004969; F:histamine recept
erPro; IPR000276; GPCR_Rhodpan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agonists.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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AF325356;
AJ298292;
AY136745;
                                                                                                                                                                                                                                                                                                                                   AF307973;
AF312230;
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Q4G016 ID Q4A AC Q4 DT 13 DT 13

Q4G016 HUMAN Q4G016; 13-SEP-2005 (13-SEP-2005 (13-SEP-2005 (

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TOPO_DOM
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PRINTS; PR01726; HISTAMINEH4R.

PROSITE; P800237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00263; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;

Receptor; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008102; Histamnrecept_H4.
PANTHER; PTHR19266:SF82; Histamnrecept_H4;
Pfam; PF00001; 7tm_1; 1.
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                                                          LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
                                                                                                     STEVPASFHSERORRKSSLMFSSRTKMMSNTIASKMGSFSQSDSVALHQREHVELLRARR
                                                                                                                                                                                        SYRTOHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF
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             CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                                                                                                LEFVIPVILVAY FNMNIYMSLMKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA
                                                                                                                                                      LEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA
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 CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                          LAKSLAILLGVFAVCMAPYSLFTIVLSFYSSATGPKSVMYRIAFMLQWFNSFVNPLLYPL
                                                                                      STEVPASFHSERORRKSSLMFSSRTKMNSNTIASKMGSFSOSDSVALHQREHVELLRARR
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100.0%; pr
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                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
S-palmitoyl cysteine (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
By similarity.
A -> V (in Ref. 1).
H -> R (in Ref. 1).
Coordinates and coordinates are a coordinates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (Potential).
Cytoplasmic (Potential).
2 (Potential)
2 (Potential)
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
4 (Potential)
5 (Potential)
Extracellular (Potential).
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Cytoplasmic (Potential).
7 (Potential).
Extracellular (Potential).
17 (Potential).
                                                                                                                                                                                                                                                                                                                      Score 2024; DB 1;
Pred. No. 1.3e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular (Potential).
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  390
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RC MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Halter J., Hulyk S.W.,

RA Halter J., Hulyk S.W.,

RA Balkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
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Best Local S
Matches 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Synthetic constructs;
NIH MGC Project;
Submitted (APR-2004) to the I
EMBL; BC069136; AAH69136.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Name=HRH4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S..
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                                                                                                                                                                                                                                                                                                                      SYRTQHTGVLKIVTLMVAVMVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF 180
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                                                                                               LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
 CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                       LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.3e-135;
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RX MEDILINE 211051319; Pubmed=11179435;
RA RAUSERT L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch K.R., Setola V., Lee D.K., Cheng R.,
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
RA Nguyen T., Lee S.P., Lynch B.L., O'Dowd B.F.;
Ra Nguyen T., Lee D., Lynch B.L., O'Dowd B.F.;
Ra Nguyen T., Lee D., Lynch B.L., O'Dow
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homini
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=21106319; Pu
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CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                  CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
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Pred. No. 4.9e-135;
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01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
Histamine H4 receptor.
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InterPro; IPR008102; Histamnrecept_H4.
PANTHER; PTHR19266:SF82; Histamnrecept_H4; 1.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida
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-- SUBCELLULAR LOCATION: Integral memorane
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GO:0016020;
GO:0004872;
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GO:0007166;
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KRFQKAFLKIFCLKKQSTLS-HNRSTSS
                KRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                            RSLAILLGVFAICWAPYSLLTITRSVYPTNPFPSTAVYKFAFWLQWFNSCVNPFLYPLCH
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Belongs to the G-protein coupled rec
BAB83078.1; -; mRNA.
C:integral to membrane; IEA.
C:membrane; IEA.
F:receptor activity; IEA.
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P:G-protein coupled receptor protein signalin.
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72.9%;
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Pred. No. 6.7
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L. No. 6.7e-94;
L. No. 6.7e-94;
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Q91ZY1;
01-DEC-2001
01-DEC-2001
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PFAM, PF00001; 7tm 1; 1
PRINTS; PR000237; GFCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transcucer; 391 AA; 44023 MW; C707BA6E39CFED41 CRC64;
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GO; GO:0016021; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0001804; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; I
GO; GO:0007186; P:G-protein coupled receptor protein
GO; GO:0007186; P:G-protein coupled receptor protein
GO; GO:0007186; P:G-protein coupled receptor protein
InterPro; IPR002776; GPCR, Rhodpsn.
InterPro; IPR008102; Histamnrecept_H4.
InterPro; IPR008102; Histamnrecept_H4.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
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                                                                                     PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG
                                                                                                               SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA
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Last annotation update)
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Pred. No. 2.9e-92;
0; Mismatches 77;
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Q91ZY2;
Q1-DEC-2001 (
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InterPro; IPR008102; Histamnrecept_H4.
PANTHER; PTHR19266:SF82; Histamnrecept_H4; 1.
Pfam; PR00001; 7tm 1; 1.
PRINTS; PR00237; GPCKRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 391 AA; 44249 MW; 59EC73CB5214C5E0 CRC64;
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MGI; MG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognat
Muridae; Murinae; Mus.
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(MGI:2429635; Hrh4.
G0:0005615; C:extracellular space; TAS.
G0:0005687; C:integral to plasma membrane;
G0:0005624; C:membrane fraction; IDA.
G0:0005624; C:membrane receptor activity;
G0:0004959; P:inflammatory response; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                              MLLEFLLPVISVAYFNVQIYMSLMKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                                                                                                                                                                                                                                                                     SYRTOHTGVLKIVTLAVAVAVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                                                                           RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPLLY
                                                                                                                                                                                                                                                             SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
                                                                                                                                                                                                                                                                                                             SYRACHTGIMKIVACMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
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                                                                                                                                                 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG
                                                                                                                                                                    SASTEVPASFHSERORRKSSLMFSSRTKYMNSNTIASKYGSFSQSDSVALHQREHVELLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWENSFVNPFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.1%;
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Last
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Pred. No. 1e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP LIU C., Wilson S., Kuei C., Lovenberg T.W.;
RRA LIU C., Wilson S., Kuei C., Lovenberg T.W.;
RRA LIU C., Wilson S., Kuei C., Lovenberg T.W.;
RRA LIU C., Wilson S., Kuei C., Lovenberg T.W.;
RRA LIU C., Wilson S., Kuei C., Lovenberg T.W.;
RRA LIU C., Wilson S., Kuei C., Lovenberg T.W.;
RRA LIU C., Wilson S., Kuei C., Lovenberg D., Rotelin C., Lovenberg C.
C. -!- SUBUCELLULAR LOCATION: Integral membrane protein (By similarity).
C. -!- SUBUCELLULAR LOCATION: Integral to the G-protein coupled receptor 1 family.
RGO; GO:0016020; C:membrane; IEA.
RGO; GO:0016020; C:membrane; IEA.
RGO; GO:00014872; F:receptor activity; IEA.
RGO; GO:0001844; F:rhodopsin-like receptor protein signalin. . ; IEA.
RGO; GO:0001584; F:rhodopsin-like receptor protein signalin. . ; IEA.
RGO; GO:0007165; P:G-protein coupled receptor; IEA.
RGO; GO:0007165; P:G-protein coupled recept H4.
RRANTHER; PTHR19266:SF82; Histamnrecept H4.
RRANTHER; PTHR19266:SF82; Histamnrecept H4; 1.
RRANTHER; PTHR19266:SF82; Histamnrecept H4; 1.
RRANTHER; PTHR19266:SF82; Histamnrecept H4; 1.
RRANTHER; PRO1726; HISTAMINEH4R.
RRR PRINTS; PR01726; HISTAMINEH4R.
RR PROSITE; PS00237; GPCRRHODOPSN.
RRINTS; PR01726; HISTAMINEH4R.
RR PROSITE; PS00237; GPCREIN RECEP F1_1; 1.
RR PROSITE; PS00237; GPCREIN RECEP F1_2; 1.
RR PROSITE; PS00237; GPCREIN RECEP F1_2; 1.
RR PROSITE; PS00237; GPCREIN RECEP F1_2; 1.
RR G-protein coupled receptor; Receptor; Transmembrane.
RR G-protein coupled receptor; S1AF32FDSF1C3E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 253; Conserv
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Q91ZY3
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Mammalia; Eutheria;
Hystricognathi; Cavi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine H4 receptor.
Cavia porcellus (Guinea pig).
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                  OHTGVLKIVTLMVAVMVLAFLVNGPMILVSESMKDEGSECEPGFFSEMYILAITSFLEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAIAIPLYIPSSLTYWTSGKQACVFWLITDYLLCTASVYNIVLISYDRYQSVSNAVWYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVISIPLYIPHTLFEWDFGKBICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFV
                                               RFQKAFLKILPVRRQSTP-PHNRSIST
                                                                                                                                SLAILLAAFAICWAPYSLTTVIYSFFPERNLTKSTWYHTAFWLQWFNSFVNPFLYPLCHK
                                                                                                                                                                    SLAILLGVEAVCWAPYSLETIVLSFYSSATGPKSVWYRIAFWLQWENSFVNPLLYPLCHK
                                                                                                                                                                                                                TTASLGSDKSRRKSSLLFSIRAYKNSNVIASKMGFI
                                                                                                                                                                                                                                                                                              IPILLVAYFSAHIYWSLWKREKLSRCLSHPVLPSDSSSSDHGHSCRQDPDSRATLPARKE
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                                                                                    REOKAFLKIFCIKKOPLPSQHSRSVSS
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iidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.1%; Score 1318.5;
65.4%; Pred. No. 1.66
tive 48; Mismatches
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1.6e-85;
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DR InterPro; IPR008102; Histamnrecept_H4.

PR PANTIHER; PTHR19266:SF82; Histamnrecept_H4; 1.

PR PANTIS; PR00001; 7tm 1; 1.

R PRINTS; PR00237; GFCRRHODOPSN.

R PRINTS; PR01726; HISTAMINEH4R.

R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

1 G_protein coupled receptor; Receptor; Transducer; Transon_TER

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NON_TER 175 175
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Q6J9J5 PANTR |
Q6J9J5;
                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Histamine receptor H4 subtype (Fragment).
Gorilla gorilla (gorilla).
Eukaryota, Metazoa; Chordata, Craniata, Vert
Mammalia; Eutheria; Euarchontoglires; Primat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 14:845-851(2004).

EMBL; AY56149; AAF45507.1; -; Genomic DNA.

EMBL; AY561621; C:integral to membrane; IEA.

GO; GO:0016021; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protesin coupled receptor protein signalin.

GO; GO:0007185; P:signal transduction; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Histamine receptor H4 subtype (Fragment).
Pan troglodyces (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15123584; DOI=10.1101/gr.1891104; Zhang J., Wang X., Podlaha O.; "Testing the chromosomal speciation hypothesis
                NUCLEOTIDE SEQUENCE.
PubMed=15123584; DOI=10.1101/gr.1891104.
                                                                                                                                                                                                                                                                                                                                             Q6J9J4 9PRIM PRELIMINARY;
Q6J9J4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                  NCBI_TaxID=9593;
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  J., Wang X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSFYSSATGPKSVWYRIAFWLQWENSFVNPLLYPLCHKREQKAFLKIFCIKKQPL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWAPYSLFTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLSRCOSHPGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASLHSERORXKSSLMFSSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 AA;
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19825 MW;
     Podlaha
                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 889; DB 2; I
Pred. No. 2.1e-55;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E5961FDAC315182F CRC64;
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                                                                                                                                                                 Hominidae;
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RESULT 10
Q865E1_MACMU
Q865E1_MACMU
Q865E1_MAC
Q860EMAC
Q86EMAC
Q8
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-!- SIMILARITY: Belongs to the G-protein coupled recept
EMBL; AY231164; AAO63757.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:histamine receptor activity; IEA.
GO; GO:0001584; F:hedopain-like receptor activity; IEA.
GO; GO:0001584; F:hedopain-like receptor activity; IEA.
GO; GO:0001585; P:nesignal transduction; IEA.
InterPro; IPR000276; GPCR_Rhodpan.
InterPro; IPR0003980; H3_receptor.
PFANNTS; PR010271; HSTRMINEH3R.
PRINTS; PR010237; GPCRRHODDESN.
PRINTS; PR010237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q865E1_MACMU PRELIMINARY;
Q865E1;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Histamine receptor H3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm 1; 1.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01726; HISTAMINEH4R.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 14:845-851(2004).

EMBL; A7561470; AAT45508.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001594; F:rhodopsin-like receptor activity;

GO; GO:0001594; P:g-protein coupled receptor protein

GO; GO:0007186; P:g-protein coupled receptor protein

GO; GO:0007185; P:gignal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Mammalia; Eutheria; Euarchontoglires; Primates;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; Receptor; NON TER 1 1 1 1 NON TER 174 174 174 SEQUENCE 174 AA; 19713 MW; 4038B74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR008102; Histamnrecept_H4.
PANTHER; PTHR19266:SF82; Histamnrecept_H4;
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Yao B.B., Sharma R., Cassar S., Esbenshade T.A., Submitted (FEB-2003) to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=HRH3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 KMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWAPYSLFTIV
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.; 19713 MW;
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Last sequence update)
Last annotation updat
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Pred. No. 6.5e-55;
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rane protein (By similarity).
coupled receptor 1 family
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RESULT
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                                                                                         J. Pharmau...
[2]
[2]
NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2...
NUCLEOTIDE STRIBLE SEQUENCE (ISOFORMS 1 AND 2...
TISSUE-Corpus striatum; PubMed=11130725; DOI=10.1038/35048583;
MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
MEDLINE=210167325; PubMed=11130725; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Hypothalamus;
MEDLINE-20330707; PubMed-10869375;
Lovenberg T.W., Pyati J., Chang H., Wilson
"Cloning of rat histamine H3 receptor revea
"Cloning of rat histamine H3 receptor revea
"Change of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRH3_RAT STANDARD;
090YNB; 090YNF; 090YNF;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
10-MAY-2005 (Rel. 47, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
Muroidea; Muridae; Murinae; Rattus.
MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
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    NUCLEOTIDE SEQUENCE (ISOFORMS
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GO; GO: UV//LIV
InterPro; IPR000276; GPCR_Rhoqps...
InterPro; IPR0003980; H3_receptor.
InterPro; IPR0003980; H3_receptor.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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Lovenberg T.W., Roland B.L., Wilson S.J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the
                                                                                                                                                                                                                                                                                                                                                 EMBL;
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GO:0007194; P:negative regulati
GO:0007194; GPCR Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             as long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                 L; AFC37919; AAF62086.1; -; mRNA.
L; AY009370; AAK02069.1; -; mRNA.
L; AB015646; BAA88765.1; -; mRNA.
L; AB015646; BAA88766.1; -; mRNA.
L; AB015646; BAA88767.1; -; mRNA.
L; AB015646; BAA88768.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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SUBCELLULAR LOCATION: Integral membrane protein
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IsoId=Q9QYN8-1; Sequence=Displayed;
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RESULT 12
HRH3 MOUSE
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AC P58406;
DT 28-FEB-2003
DT 28-FEB-2003
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DA Histamine H:
GN Name-Hrh3;
OS Mus musculuu
OC Eukaryota; I
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Best Local Similarity
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
Muroidea; Muridae; Murinae; Mus.
  STRAIN=CD-1;
Coge F., Rique H.,
Galizzi J.-P.;
                                                        NCBI_TaxID=10090;
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Missing (in isoform 3 and isoform 4)
/FTId=VSP_001888.
Missing (in isoform 2).
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PR00237; G PROTEIN RECEP P1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
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                                                                                               EFVIPVILVAYFNMNIY------WSLWKRD
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                                                    HLSRCQSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS
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Pred. No. 1.8e-43;
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PRINTS; PR00237; GFCRMINDEBJR.
PRINTS; PR01471; HISTAMINDEBJR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 445 AA; 48541 MW; B8D406E29E1F3C5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=22592891; PubMed=12706455; DOI=10.1016/S0014-2999(03)01635-2;
Chen J., Liu C., Lovenberg T.W.;
"Molecular and pharmacological characterization of the mouse histamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI; MGI:2139279; Hrh3.
GO; GO:0016021; C:integral to membrane; InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein -!- SIMILARITY: Belongs to the G-protein coupled recEMBL; AY142145; AAN14941.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H(3) receptor."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVISIF
                                                                                                                                                                                                                                                 RRAVRKMALVMVLAFILYGPAIL---SWEYLSGGSSIPEG-HCYAEFFYNWYFLITASTL
                                                                                                                                                                                                                                                                                                                                                                                                               LYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGV 129
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                                                                              HLSRCQSH---
                                                                                                                                      EFFTPFLSVTFFNLSIYLNIQRRTRLRLDGGREAGPEPPPDAQPSPPPAPPSCWGCWPKG
                                                                                                                                                                                          BEVIPVILVAYENMNIY----
                                                                                                                                                                                                                                                                                                                                                             LÝVÞYVLTGRWTFGRGLCKLWLVVDYLLCASSVFNÍVLÍSYDRFLSVTRAVSÝRAQQGDT
                          HGEAMPLHRYGVGEAGPGVETGEAGLGGGSGGGAAASPTSSSGSS
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                                                                              ----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS
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Pred. No. 1.8e-43;
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Best Local S
Matches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "photoperiodic Regulation of Histamine H3 Receptor and VGF Messenger Ribonucleic Acid in the Arcuate Nucleus of the Siberian Hamster."; Endocrinology 146:1930-1939(2005).

-i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; AY855070; AAW55866.1; -; mRNA.
GO; GO:0006021; C:integral to membrane; IEA.
GO; GO:000621; C:integral to membrane; IEA.
GO; GO:0004969; F:histamine receptor activity; IEA.
GO; GO:0004584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; I GO; GO:0007185; P:signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01471; HISTAMINEB3R.

PROSITE; P800237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; P850262; G_PROTEIN_RECEP_F1_2; 1.

G-pxotein coupled receptor; Receptor; Transmembrane.

SEQUENCE 445 AA; 48488 MW; DD8969E9D192BF22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2005 (TrRMBLrel. 30, Created)
10-MAY-2005 (TrRMBLrel. 30, Last sequence update)
10-MAY-2005 (TrRMBLrel. 30, Last samotation update)
10-MAY-2005 (TrRMBLrel. 30, Last annotation update)
11-MAY-2005 (TrRMBLrel. 30, Last sequence update)
11-MAY-2005 (TrRMBLrel. 30, Last samotation u
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Barrett P., Ross A.W., Balik A., Littlewood P.A., Mercer J.
Moar K.M., Sallmen T., Kaslin J., Panula P., Schuhler S., E
Ubeaud C., Morgan P.J.;
"Phorpropersiation"
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InterPro; IPR003980; H3_receptor.
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                                                                                                                                                                                                                                                       LYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGV 129
                                                                                                                                                                                                                       LYVPYVLTGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYRAQQGDT 149
                                                                                                                                                                                                                                                                                                                                                                   SLSTRVTLAFEMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVISIP
                                                    EFVIPVILVAYFUMNIY----
                                                                                                              RRAVQKMALVWVLAFLLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFYNWYFLITASTL
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EFFTFFLSVTFFNLSIYLNIQRRTRLRLDGAREAGPEPPPDAQPSPPPAPPSCWGCWPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 727; DB
Pred. No. 1.8e
51; Mismatches
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1.8e-43;
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HRH3_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Filot C., Cochois V., Schwartz J.-C., Arrang J.-M.;

"Cloning and cerebral expression of the guinea pig histamine H3 receptor: evidence for two isoforms.";

NeuroReport 11:755-759 (2000).

-!- FUNCTION: The H3 subclass of histamine receptors could mediate thistamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRH3_CAVPO STANDARD; PRT; 445 AA Q9JI35; Q9JI36; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation updat. Histamine H3 receptor (HH3R)
                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GFCRMINDH3R.

PRINTS; PR01471; HISTANIBH3R.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                            EMBL; AF267537; AAF78947.1; -; mRNA.
EMBL; AF267538; AAF78950.1; -; mRNA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3 receptor.
Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain; MEDLINE=20218440; PubMed=10757514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE (ISOFORMS LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                         removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=HRH3;
                                                                                                                                                                                                                                                                                     Name=Short; Synonyms=H3S;
IsoId=99JI35-2; Sequence=VSP_001880;
IISOId=99JI35-2; Sequence=VSP_001880;
IISSUE SpECIFICITY: Expressed widely and abundantly throughout the brain. Highly expressed in discrete neuronal populations such as brain. Highly expressed in discrete or cerebellar Purkinje cells. Byramidal cells in cerebral cortex or cerebellar Purkinje cells. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                              85
                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2; Name=Long; Synonyms=H3L; IsoId=Q9JI35-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane
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Search completed: March 28, 2006, 13:58:30 Job time : 235 Becs

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; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2
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APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Morse, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Unland, Shelby P.
APPLICANT: Wang, Suke
TITIE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
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US-08-444-734A-7
US-08-406-855A-22
US-09-206-899-22
US-09-206-899-22
US-09-688-415-9
US-08-467-558-10
US-09-334-698-4
US-08-228-939-4
US-08-246-855A-4
US-08-246-855A-4
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Pred. No. 1.1e-159;
Mismatches 0;
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Sequence 21, Appli
Sequence 7, Appli
Sequence 22, Appl
Sequence 25, Appl
Sequence 25, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 4, Appli
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120

60

120

300

240

180

Result No.

Score

Pred. No.

18

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NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-812-216-2
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Sequence 14, Application US/09875076
Patent No. 6869776
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
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Patent No. 6613533
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Best Local Similarity
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APPLICANT: Hedrick, Joseph A.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14
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LENGTH: 390
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TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOO50
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
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PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
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PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
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PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
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PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
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PRIOR FILING DATE: 1999-02-16
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PRIOR FILING DATE: 1999-06-29
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PRIOR APPLICATION NUMBER: 60/123,946
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61 DFFVGVISIPLYIPHTLPEWDFGKBICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV
                                                                                                                                                                           LEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSLSA 240
                                   SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF
                                                      SYRTOHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF 180
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ORGANISM: Monkey US-10-453-106-2
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SOPTWARE: PatentIn ver
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LENGTH: 445
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Patent No. 690606
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APPLICANT: Hoblweg, Rolf
TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES,
TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A] PYRAZINES AND
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEPINES
TILE REFERENCE: 6483.200-US
CURRENT APPLICATION NUMBER: US/10/453,106
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
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PRIOR APPLICATION NUMBER: Danish Application
PRIOR FILING DATE: 2002-06-06
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                                                                 VCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAFLKIF 373
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                                                                                                                                                RRKSSLMFSSRTKWNSNTIASKWGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFA 313
                                                                                                                                                                                            HGEAMPLHRYGVGEAAAGAEAGETALGGGGGGGSAASPTSSSGSSSRGTERPRSLKRGSK 325
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                                                                                                                                                                                                                                                                             EFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAGGPEPPPEAQPSPPPPPGCWGCWQKG 265
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39.2%; Pred. No. 1.7e-52;
ative 47; Mismatches 132;
                                                                                                           ---SFTQ-
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APPLICANT: Andrew D.J. Goodearl and TITLE OF INVENTION: Muscarinic Reconumber of SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LISTREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Applic Patent No. 6093545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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                          258
                                                                                                                                                                                              182
                                                                                                                                                                                                                                                                             130 LKIVTLMVAVWVLAFLVNGPMILVSESWK------DEGSECEPGFFSEWYILAITSFL 181
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SLMFSSRTKANSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        С---ІККОР 379
                                                                   HGEAMPLHRYGVGEAGPGVEAGEAALGGGSGGGAAASPTSSSGSS
                                                                                                           HLSRCOSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERORRKS 257
                                                                                                                                                                                                                                    RRAVRKMALVMVLAFILLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFYNWYFLITASTL 205
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39.1%; Pred. No. 2e-52;
tive 54; Mismatches 131; Indels
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TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROFILE REFERENCE: 06501-083001

CURRENT APPLICATION NUMBER: US/09/891,053

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: PCT/JP99/07280

PRIOR FILING DATE: 1999-12-24

PRIOR FILING DATE: 1999-12-25

PRIOR FILING DATE: 1999-12-55

PRIOR APPLICATION NUMBER: PCT/JP98/05967

PRIOR FILING DATE: 1999-12-55

PRIOR APPLICATION NUMBER: DT 11/145661

PRIOR PILING DATE: 1999-05-25

NUMBER: DG CECT TO NOCE CO.
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TYPE: PRT
CORGANISM: Rattus norvegicus
US-09-891-053-25
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Best Local Similarity 39.1%; Pred. No. 2e-52;
Matches 166; Conservative 54; Mismatches 1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
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PYTLLMIIRAACHGRCIP-DYWYETSFWLLWANSAVNPVLYPLCHYSFRRAFTKLLCPQK 431
                                            PYSLETIVLSEYSSATGPKSVWYRIAFWLQWENSEVNPLLYPLCHKREQKAELKIEC--- 374
                                                                                     SIKRGSKPSASSASLEKRMKMVSQSIT-----QRFRLSRDKKYAKSIAIIVSIFGLCWA 372
                                                                                                                                         SLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
                                                                                                                                                                                   HGEAMPLHRYGVGEAGPGVEAGEAALGGGSGGGAAASPTSSSGSS-----SRGTERPR 318
                                                                                                                                                                                                                            HLSRCQSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS 257
                                                                                                                                                                                                                                                                    EFFTPFLSVTFFNLSIYLNIQRRTRLRLDGGREAGPEPPPDAQPSPPPAPPSCWGCWPKG
                                                                                                                                                                                                                                                                                                               SLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVISIF
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Hidaka, Yusuke
Ohta, Masataka
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Nakamura, Takao
Kobayashi, Masahiko
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APPLICANT: Hoblweg, Rolf
TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES,
TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A] PYRAZINES AND
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEPINES
FILE REFERENCE: 6483,200-US
CURRENT APPLICATION NUMBER: US/10/453,106
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
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: TYPE: PRT
: ORGANISM: Rat
US-10-453-106-3
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US-08-985-090-2
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        Sequence 2, Application US/08985090 Patent No. 5885893 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                        375
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                                                                                                                                                                                                                                                                                                                                        SLKRGSKPSASSASLEKRMKMVSQSIT-----QRFRLSRDKKVAKSLAIIVSIFGLCWA
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Best Local :
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 35.8%; Score 724; DB 1; Length 445; Local Similarity 38.6%; Pred. No. 5.2e-52; nes 164; Conservative 56; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 39, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/985,090 FILING DATE:
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CITY: Boston
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                                              IKKOP 379
                                                                                                                                                                                                                                 SLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
                                                                                                                                                                                                                                                                            HGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSVASPTSSSGSS-----SRGTERPR 318
                                                                                                                                                                                                                                                                                                                        HLSRCQSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS
                                                                                                                                                                                                                                                                                                                                                                      EFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPPPGCWGCWQKG 265
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LKIQP 436
                                                                                                                                                                                SIKRGSKPSASSASIEKRMKMVSQSFT-----QRFRISKDRKVAKSLAVIVSIFGLCWA
                                                                                         PYTLLMITRAACHGHCVP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKLLCPQK 431
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28 State Street
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US-09-165-543-2
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Best Local Similarity 38.6%;
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INFORMATION FOR SEQ ID NO:
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LENGTH: 445 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comppatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
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                                    PYSLFTIVLSFYSSATGEKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAFLKIFC---
                                                                           SIKRGSKPSASSASIEKRMKMVSQSFT-----QRFRLSRDRKVAKSIAVIVSIFGICWA
                                                                                                                SLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA
                                                                                                                                                                                          HLSRCQSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS 257
                                                                                                                                                                                                                                 EFFTPFLSVTFFNLSTYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPPPGCWGCWQKG
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(617)742-4214
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Pred. No. 5.2e-52;
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; Sequence 7, Application US/09642855; Patent No. 6413743; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
                                                                                  RESULT 11
US-09-642-855-7
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LENGTH: 445
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
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APPLICANT: Huvar, Arne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR ITLE OF INVENTION: SUBTYPE
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RESULT 12
US-09-642-514-7
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                                                                                                                                                                                                                                                                     Sequence 7, Application US/09642514 Patent No. 6437100
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                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE TITLE OF INVENTION: SUBTYPE FILE REFERENCE: ORT1190 CURRENT APPLICATION NUMBER: US/09/642,514 CURRENT FILING DATE: 2000-08-21 PRIOR APPLICATION NUMBER: US 09/167,354 PRIOR FILING DATE: 1998-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
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APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
                                                                                                                                                         APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
                                                                                                                                                                                                     APPLICANT: Lovenberg, Timothy APPLICANT: Erlander, Mark
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                         RECEPTOR OF
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US-09-642-514-7
                                                                                                                PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
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Best Local Similarity
Matches 164; Conserv
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LENGTH: 445
TYPE; PRT
ORGANISM: Artificial Sequence
PEATURE:
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
-09-642-852-7
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/642, CURRENT FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                        FILE REFERENCE: JWW
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAAWTAVLAALMALLIVATVLGNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIP
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Sequence 1, Application US/10453106

Patent No. 6906060

GENERAL INFORMATION:
APPLICANT: Peschke, Bernd
APPLICANT: Hohlweg, Rolf
ITILS OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES,
ITILE OF INVENTION: OCTAHYDROPYRLDO[1,2-A] PYRAZINES AND
ITILE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEPINES
FILE REFERENCE: 6483.200-US
CURRENT APPLICATION NUMBER: US/10/453,106
CURRENT APPLICATION NUMBER: US/03-06-03
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR PILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-06
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US-10-453-106-1
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US-10-453-106-1
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Best Local Similarity
Matches 164; Conserv
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Best Local Similarity 38.6%; Pred. No. 5.2e-52;
Matches 164; Conservative 56; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                        LYIPHTLF-EWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGV 129
LYVPYVLIGRWIFGRGLCKLWLVVDYLLCISSAFNIVLISYDRFLSVTRAVSYRAQQGDT 149
                                                                                          SAAWTAVLAALMALLIVATVLGNALVMLAFVADSSLRTONNFFLLNLAISDFLVGAFCIP
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US-09-949-016-10930
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SOFTWARE: FASCEQ for Windows Version 4.0
SEQ ID NO 10930
LENGTH: 449
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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-09-949-016-10930
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-20
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CURRENT FILING DATE: 2000-04-14
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                         375 IKKQP 379
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Search completed: March 28, 2006, 14:00:09
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Result
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3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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US-10-255-567A-629
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US-10-696-673-2
US-10-696-673-2
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US-10-696-673-2
US-10-626-144-2
US-10-626-146-2
US-10-626-398-2
US-10-626-398-2
US-10-756-149-4702
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FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-812-216-2
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Publication No. US20020098539A1
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APPLICANT:
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APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsma, Frederick
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                            STEVPASFHSERQRRKSSIMFSSRTKVMSNTIASKMGSFSQSDSVALHQREHVELLRARR
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US-09-910-411-2
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PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR PPLICATION NUMBER: 09/431,898
PRIOR FILING DATE: 1999-11-02
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SEQ ID NO 2
LENGIH: 390
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APPLICANT: Bergema, Derk
APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiatong
APPLICANT: Michalovich, David
Sequence 14, Application US/09875076
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Best Local Similarity
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TITLE OF INVENTION: ACROS, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C1
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2001-07-20
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301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL 360
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CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR PPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 05/123,946
PRIOR APPLICATION NUMBER: 05/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR PILING DATE: 1999-05-28
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Matches
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LENGTH: 390
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GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Tiaw,
                                                                                                                                                                                                                                                                                                                         Query Match
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PRIOR APPLICATION NUMBER: 60/136,567
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
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PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
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PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
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121 SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAITSF 180
                                                                                                                                                                                                                                                                          390;
                                                        61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV
                                                                                                                                                                                              1 MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
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                                                                                                                                                               MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
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Pred. No. 1.4e-173;
Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/876,252
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILLING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILLING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILLING DATE: 1999-02-26
PRIOR FILLING DATE: 1999-02-26
PRIOR FILLING DATE: 1999-03-12
PRIOR FILLING DATE: 1999-03-12
PRIOR PILLING DATE: 1999-03-12
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US-09-876-252-14
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APPLICANT: Lehmann-Bruinsma,
APPLICANT: Chalmers, Derek T
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Lin
APPLICANT: Dang, Huong T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09876252 Publication No. US20030018182A1
                                                                                                                                                          PRIOR
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PPLICANT: Liaw, Chen W.
ITLE OF INVENTION: Non-Endogenous Constitively Activated
                    OR APPLICATION NUMBER: 60/108,029
NR FILING DATE: 1998-11-12
NR APPLICATION NUMBER: 60/136,436
OR FILING DATE: 1999-05-28
NR APPLICATION NUMBER: 60/136,439
OR APPLICATION NUMBER: 60/136,567
OR APPLICATION NUMBER: 60/136,567
                                                                                                                                                                                                                                                                                         DR FILING DATE: 1999-03-12
RR APPLICATION NUMBER: 60/123,948
DR FILING DATE: 1999-03-12
DR APPLICATION NUMBER: 60/123,951
DR FILING DATE: 1999-03-12
DR APPLICATION NUMBER: 60/123,946
DR APPLICATION NUMBER: 60/123,946
                                                                                                                                                 APPLICATION NUMBER: 60/152,524
FILING DATE: 1999-09-03
APPLICATION NUMBER: 60/151,114
FILING DATE: 1999-08-27
FILING DATE: 1999-08-27
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APPLICATION NUMBER: 60/
FILING DATE: 1999-03-12
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Derek T.
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; TYPE: PRT
; ORGANISM: Homo s
US-09-876-252-14
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US-09-852-165-2
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Sequence 2, Application US/09852165
Publication No. US20030032784A1
GENERAL INFORMATION:
APPLICANT: Lind, Peter
APPLICANT: Sejlitz, Torsten
APPLICANT: Vogeli, Gabriel
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Best Local
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OR FILING DATE: 1999-05-28

OR APPLICATION NUMBER: 60/137,131

OR FILING DATE: 1999-05-28

OR APPLICATION NUMBER: 60/141,448

OR FILING DATE: 1999-05-28

OR APPLICATION NUMBER: 60/136,437

OR FILING DATE: 1999-05-28

OR APPLICATION NUMBER: 60/156,555

OR FILING DATE: 1999-09-29

OR APPLICATION NUMBER: 60/156,634

OR APPLICATION NUMBER: 60/156,634

OR APPLICATION NUMBER: 60/157,280

OR APPLICATION NUMBER: 60/157,280

OR APPLICATION NUMBER: 60/157,280

OR APPLICATION NUMBER: 60/157,294

OR APPLICATION NUMBER: 60/157,291

OR APPLICATION NUMBER: 60/157,291
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FILING DATE: 1999-10-01
APPLICATION NUMBER: 60/156,633
FILING DATE: 1999-09-29
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APPLICANT: Lin, Daniel Chi-Hong
APPLICANT: Zhao, Jiagang
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Tularik Inc.
TITLE OF INVENTION: NO. US20030083245A1el Receptors
FILE REFERENCE: 018781-006210US
CURRENT APPLICATION NUMBER: US/09/891,138A
CURRENT FILING DATE: 2001-06-25
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 26
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2
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                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
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TITLE OF INVENTION: No. US20030032784Alel G Protein-Coupled Receptors

FILE REFEROCE: 00231regUS

CURRENT APPLICATION NUMBER: US/09/852,165

CURRENT FILING DATE: 2001-05-08

PRIOR APPLICATION NUMBER: USSN 60/203,108

PRIOR APPLICATION DATE: 2000-05-08

UNMBER OF SEQ ID NOS: 3
FEATURE:
OTHER INFORMATION: human TGR62 G-protein coupled receptor
09-891-138A-6
                                                    LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 2, Application US/10052193

Publication No. US20020132755A1

GENERAL INFORMATION:
APPLICANT: PÉLEET, Inc.
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
FILE REFERENCE: PC10963A
CURRENT APPLICATION NUMBER: US/10/052,193
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 0101223.6

PRIOR APPLICATION NUMBER: 0101223.6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        LENGTH: 390
TYPE: PRT
ORGANISM: Homo
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100.0%; Pred. No. 1.4e-173;
7ative 0; Mismatches 0;
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100.0%; Pred. No. 1.4e-173;
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US-10-225-567A-629
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEO ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 629
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 629, Application US/1022567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES
FILE REFERENCE: 1920-4-4
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Best Local
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TYPE: PRT
ORGANISM: Homo sapiens
-10-225-567A-629
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Application US/10272983
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-14
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CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR PPLICATION NUMBER: 60/109,213
PRIOR FILING-DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR PILING DATE: 1999-02-26
PRIOR PILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
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OR FILING DATE: 1999-05-28
OR APPLICATION NUMBER: 60/136,437
OR FILING DATE: 1999-05-28
OR APPLICATION NUMBER: 60/136,439
OR FILING DATE: 1999-05-28
OR APPLICATION NUMBER: 60/136,567
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Liaw, Chen W.
Lin, I-Lin
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61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV
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LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL
                                                                               STEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARR
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RESULT 11
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APPLICANT: Peter: Beate
APPLICANT: Peter: Beate
TITLE OF INVENTION: NOVEL POLYPEPTIDE
FILE REFERENCE: PC10373B
CURRENT APPLICATION NUMBER: US/10/354,769
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 09/698,801
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: GB 9025641.4
PRIOR APPLICATION NUMBER: GB 9025641.4
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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TYPE: PRT
ORGANISM: Homo sapiens
-10-354-769-2
                                                             APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein
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FILE REFERENCE: ARENOO50
CURRENT APPLICATION NUMBER: US/10/393,807
CURRENT FILING DATE: 2003-03-21
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                                                                       Coupled Receptors
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US-10-417-820A-14

Sequence 14, Application US/10417820A Publication No. US20030229216A1 GENERAL INFORMATION:

APPLICANT: Chen, Ruoping APPLICANT: Liaw, Chen W. APPLICANT: Lowitz, Kevin APPLICANT: Chalmers, Derr APPLICANT: Behan, Dominic

INVENTION: Constitutively Activated Human

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Protein Coupled

Chalmers, Derek T. Behan, Dominic P.

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; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-14
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OR FILING DATE: 1998-11-20
OR APPLICATION NUMBER: 60/120,416
OR FILING DATE: 1999-02-16
OR APPLICATION NUMBER: 60/121,851
OR FILING DATE: 1999-02-26
OR APPLICATION NUMBER: 60/123,946
OR FILING DATE: 1999-03-12
OR APPLICATION NUMBER: 60/123,949
OR FILING DATE: 1999-03-12
OR APPLICATION NUMBER: 60/123,949
OR FILING DATE: 1999-03-12
OR APPLICATION NUMBER: 60/123,949
OR APPLICATION NUMBER: 60/123,949
OR APPLICATION NUMBER: 60/123,949
OR APPLICATION NUMBER: 60/136,436
OR APPLICATION NUMBER: 60/136,437
OR FILING DATE: 1999-05-28
OR APPLICATION NUMBER: 60/136,436
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FILING DATE: 1999-05-28
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                                                                                                                                   LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPL 360
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CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
                                           CHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
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                                     Sequence 2, Application US/10349253A Publication No. US20040043393A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
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TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2003-04-16
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FILING DATE: 1998-11-20
APPLICATION NUMBER: 60/123,944
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ILING DATE: 1999-03-12
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Pred. No. 1.4e-173;
D; Mismatches 0;
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PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/431,898
                                                                                                                                                                                        Sequence 2, Application US/10696673 Publication No. US20040105846A1 GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Sejlitz, Torsen
APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G
FILE REFERENCE: PHRW0025-101/00231EGUS.1 DV1
CURRENT APPLICATION NUMBER: US/10/696,673
CURRENT FILING DATE: 2003-10-28
                                                                                                      APPLICANT: Pharmacia & Upjohn
APPLICANT: Lind, Peter
APPLICANT: Sejlitz, Torsen
APPLICANT: Vogeli, Gabriel
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TITLE OF INVENTION: AXOR35, A G-Protein Coupled
FILE REFERENCE: GP70655-2C2
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TYPE: PRT
ORGANISM: Homo sapien
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Michalovich,
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; PRIOR APPLICATION NUMBER: US 60/203,108; PRIOR FILING DATE: 2000-05-08; PRIOR APPLICATION NUMBER: US 09/852,165; PRIOR FILING DATE: 2001-05-08; NUMBER OF SEQ ID NOS: 3; SOPTWARE: Patentin version 3.2; SEQ ID NO 2; LENGTH: 390; TYPE: PRT; ORGANISM: Homo sapiens
TITLE OF INVENTION: Constitutively Activated Human G F
TITLE OF INVENTION: Receptors
FILB REFERENCE: 7. US29.COM
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
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US-10-723-955-14
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APPLICANT: Behan, Do
APPLICANT: Chalmers
APPLICANT: Lin, I-L
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Matches
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Publication No. US20040110238A1
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Liaw, Chen W
Lehman-Bruinsma, Karin
Lowitz, Kevin P.
Lowitz, Huong T.
Chen, Ruoping
Gore, Martin
White, Carol
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-955-14
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PRIOR PILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
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NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
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Search completed: March 28, 2006, 14:03:02 Job time: 167 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDS5/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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10	377.5	18.7	429	7	US-11-127-877-51		51, Appl
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12	375	18.5	353	σ		Sequence	10, Appl
13	372	18.4	487	7	US-11-249-847-582		582, App
14	348.5	17.2	400	σ	US-10-499-210-2	Sequence	2, Appli
15	344	17.0	350	7	US-11-165-024-3	Seguence	3, Appli
16	314.5		446	7	US-11-166-412-67	Sequence	67, Appl
17	314	15.5	345	7	US-11-174-816-15	Sequence	15, Appl
18	314		345	7		Sequence	70, Appl
19	313	15.5	712	σ	US-10-521-162-12	Sequence	12, Appl
20	310	15.3	365	σ	US-10-875-716-9	Sequence	9, Appli
21	300.5	14.8	475	თ	US-10-877-346-48		48, Appl
22	299.5	14.8	345	7	-751-1		•
23	298	14.7	345	7	US-11-174-816-59	Sequence	59, Appl
24	298	14.7	345	7	US-11-174-819-78		78, Appl
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: G-PROTEIN CO-0236 USN NUMBER: US/10 2005-10-04 UUMBER: US/10/ 2003-03-28 UUMBER: PCT/US 2001-09-28 UUMBER: US 60/ 2000-11-03 UUMBER: US 60/ 2000-11-13 UUMBER: US 60/ 2000-11-03 UUMBER: US 60/ 2000-10-20 000-11-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20 000-10-20	ication US/11241956 US20060024792A1 US20060024792A1 UTTE GENOMICS INC.; E UTL Richard C.; CHAM EDHI, Ameena R.; HAP EKUMAR, Jayalaxmi; T ERUTON, Michael B.; ELLIC DYMON, Neil; KHAN, F C, Henry; LU, Yan; C, Henry; LU, Henry; LU, Henry; C, Henry; LU, Henry; LU, Henry; C, Henry
WIN COUPLED RE WIN W/11/241,95 10-04 105/10/398,036 PCT/US01/30661 128 105 60/245,855 108 60/240,589 113 105 60/249,343 105 60/249,343 105 60/247,587 105 60/247,587 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900 105 60/245,900	/1124195 /1241 /792A1 S INC.; S INC.; A R.; HA A R.; HA A RA; HA JA RA; JA ELLI JA J
US/11/241,956 0-04 10-04 11/10/398,036 18/10	12419) 2A1 INC.; ; CH. R.; CH. R.; H. Axmi; el B. el B. ; ELL; KHAN, Yan; Yan; S.; I B.; II B.; II
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TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES,
TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A] PYRAZINES AND
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEPINES
FILE REFERENCE: 6483.200-US
CURRENT APPLICATION NUMBER: US/11/115,564
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR APPLICATION NUMBER: US 60/387,047
PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
PRIOR FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 168; Conserv
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Monkey
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US-11-115-564-3
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CURRENT FILING DATE: 2005-04-27

PRIOR APPLICATION NUMBER: US 60/387,047

PRIOR PILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863

PRIOR FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.2

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35...
166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Peschke, Bernd
APPLICANT: Hohlwey, Rolf
APPLICANT: Hohlwey, Rolf
TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES
TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A] PYRAZINES AND
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEFINES
FILE REFERENCE: 6483.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/11115564
Publication No. US20050267116A1
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                                                                                                                                       HGEAMPLHRYGVGEAGÞGVEAGEAALGGGSGGGAAASPTSSSGSS-----SRGTERPR
                                                                                                                                                                            HLSRCQSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS 257
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                                                     SIKRGSKPSASSASLEKRMKMVSQSIT-----QRFRLSRDKKVAKSLAIIVSIFGLCWA
                                                                                                SLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
                                                                                                                                                                                                                     EFFTFFLSVTFFNLSIYLNIQRRTRLRLDGGREAGPEPPPDAQPSPPPAPPSCWGCWPKG 265
                                                                                                                                                                                                                                                              EFVIPVILVAYFUMNIY-----
                                                                                                                                                                                                                                                                                                   RRAVRKWALVWVLAFILLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFYNWYFLITASTL 205
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39.1%; Pred. No. 2.4e-57;
tive 54; Mismatches 131; Indels
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Sequence 1, Application US/1111564

Publication No. US20050267116A1

GENERAL INFORMATION:

PAPPLICANT: Peschke, Bernd

APPLICANT: Peschke, Bernd

APPLICANT: Hohlweg, Rolf

TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES,

TITLE OF INVENTION: OCTAHYDROPYRIOO[1,2-A] AZEPINES

TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEPINES

TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] AZEPINES

CURRENT EFFERNCE: 6483.200-US

CURRENT APPLICATION NUMBER: US/11/115,564

CURRENT FILING DATE: 2005-04-27

PRIOR APPLICATION NUMBER: US 60/387,047

PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06
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; TYPE: PRT
; ORGANISM: Homo S
US-11-115-564-1
RESULT 5
US-11-124-368A-183
; Sequence 183, Application US/11124368A
; Publication No. US20050287559A1
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                  SLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA
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                                                                                                                                                                                                                                                                                                                                                                                               HLSRCQSH-----PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKS
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38.6%;
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Pred. No. 6.6e-57;
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Sequence 54, Application US/11127877; Sequence 54, O. US20050287565A1; GENERAL INFORMATION:
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    APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound
TITLE OF INVENTION: Amyloid-Beta Protein Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363
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; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-183
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APPLICANT: Mames J. Devlin
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REPERENCE: CLO01524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
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                                                                                                                            TVNPVCYALCNKTFRTTFKMLLLCQCDKKKRRKQQYQQRQS
                                                                                                  RMSLVKEKKAAQTLSAILLAPIITWTPYNIMVLVNTFCDSCI-PKTFW-NLGYWLCYINS
                                                                                                                                                                                                    SFSKLPIQLESAVDTAKTSDVNSSVGKSTATLPLSFKEATLAKRFALKTRSQ---ITKRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTI----LYWRIYKETEKRTKELAGLQASGTEAETENFVHPTGSSRSCSSYELQQQSMKR 302
                                                                                                                                                                                                                                                 SFHSERORRKSSLMFSSRTKMNSN-----
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22.6%; Pred. No. 6.9e-29;
tive 95; Mismatches 150
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Assays

For

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CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOPTWARE: PATENTIAN VETSION 3.3
SEQ ID NO 54
LENGTH: 590
TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-877-54
                                                                                                                                                                           ## Sequence 42, Application US/11127877

## Publication No. US20050287565A1

## GENERAL INFORMATION:

## APPLICANT: Merchiers, Pascal G.

## APPLICANT: Merchiers, Marcel

## APPLICANT: Spittaels, Koenraad F. F.

## APPLICANT: Laenen, Wendy
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US-11-127-877-42
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Best Local Similarity 22.6%;
Matches 118; Conservative 95
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/503,948
PRIOR APPLICATION NUMBER: 60/603,948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RMSLVKEKKAAQTLSAILLAFIITWTPYNIMVLVNTFCDSCI-PKTFW-NLGYWLCYINS 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TVNPVCYALCNKTFRTTFKMLLLCQCDKKKRRKQQYQQRQS 578
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Pred. No. 6.9e-29;
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GENERAL INFORMATION:

APPLICANT: Merchiers, Pascal G.

APPLICANT: Hoffmann, Marcel

APPLICANT: Hoffmann, Marcel

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Laenen, Wendy

ITITLE OF INVENTION: Methods, Compositions and

ITITLE OF INVENTION: Methods, Compositions and

ITITLE OF INVENTION: Methods, Compositions and

ITITLE OF INVENTION METHOD BOSA

CURRENT FILING DATIS: 200-8 USA

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: 60/570,352

PRIOR APPLICATION NUMBER: 60/603,948

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOFTWARE: Patentin version 3.3
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                SEQ ID NO 41
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 590
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466
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                                                                                                                                                                                                                                          and Compound Assays For Inhibiting
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TYPE: ERT
; ORGANISM: Rhipicephalus sanguineus
US-10-521-162-40
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Publication No. US20050287529A1

GENERAL INFORMATION:
APPLICANT: Brandt, Kevin S.

TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: PROTEINS AND USES THEREOF

FILE REFERENCE: FC-11-FCT

CURRENT APPLICATION NUMBER: US/10/521,162

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: 60/319,402

PRIOR APPLICATION NUMBER: 60/319,402

PRIOR TILING DATE: 2003-07-17

PRIOR PRIOR FILING DATE: 2003-07-17
                                                                                                                                                                    Matches
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 40
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/426,601
PRIOR FILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 I-PNTVW-TIGYWLCYINSTINPACYALCNATEKKTF 451
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                                                                                                                                                                  115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 RGRL-----SSRRSLSASTEVPASF--- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 PLTYPVKRT---TKWAGMWIAAAWVLSFILWAPAILF---WQFIVGVRTVEDGECYIQFFS
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TLFE-WDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGVLKIVT 134
                                                                       VALEFVIGSINGLVIFGNILVIIAVLASTKLRTVINYFVVSLAVADLSVGLTVLPYSIVL 79
                                                                                                                        VTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVISIPLYIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGPKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQNIVARKIVKMIKQPAKKKPPPSREKKVTRTILAILLAFIITWAPYNVMVLINTFCAPC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVALHQREHVELL------RARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDDEITQDENTVSTSLGHSKDENSKQTCIRIGTKTPKSDSCTPTNTTVEVVGSSGQNGDE
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                                                                                                                                                                    Conservative
                                                                                                                                                               19.0%; Score 384.5; DB 6; Length 480; 25.9%; Pred. No. 1.2e-26; ative 67; Mismatches 161; Indels 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSERORRKSS-LMFSSRTKMN-----SNTIASKMGSFSQS--D 283
                                                                                                                                                                       Indels 101;
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Best Local Similarity
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TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
PRIOR FILING DATE: 2004-08-24
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                                                                                                                                                                    124 --TOHTGVLKIVTLMVAVWVLAFLVN-GPMILVSESWKDEGSE----C---EPGFFSEW 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
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                                                                                                                                                                                                                                                                                                              21 VNIŠKAILĖGVILGGĖILĖGV-LGNILVILSVACHRHLHSVTHYYIVNLAVADLLLITSTV 79
                                                                                                                                                                                                                                                                                                                                                        10 LSLSTRVTLAFFM-SLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVIS 68
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                                                                            YIL--AITSFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRG 230
                                                                                                                                                                                                                     LPF---SAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISIDRYIGVSYPLRYPT 136
                                                                                                                                                                                                                                                               IPLYIPHTLEE----WDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYR- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAINPLIYVLVSKOFRLAFKRILC 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoffmann, Marcel
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                                                                                                                                                                                                                                                                                                                                                                                                           18.7%; Score 377.5; DB 7; 27.6%; Pred. No. 4.6e-26; tive 73; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                           Indels 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 429;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-50
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US-11-127-877-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50, Application US/11127877 Publication No. US20050287565A1 GENERAL INFORMATION:
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TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
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PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                             137 IVTQRRGLM----ALLCVWALSLVISIGPLF----GWRQPAPEDETICQINEEPG----- 183
                                                                                                                                                                                                                                                                                                                                                                                      124 --TOHTGVLKIVTLMVAVWVLAFLVN-GPMILVSESWKDEGSE----C---EPGFFSEW 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NSFVNPLLYPLCHKRFQKAF---LKIFCIKKQPLPSQHS 385
                                                                                                                                                                      LKSGLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHF----
                                                                                                                                                                                                               RLSS-RRSLSASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQ 289
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                                                                                 ---LKFSREKKAAKTLGIVVGCFVLCWLPFFLVMPIGSFFPDFK-PSETVFKIVFWLGYL 317
                                                                                                                            REHVELLRARRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWF 349
                                                                                                                                                                                                                                                                                                   YIL--AITSFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRG 230
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NSCINPITYPCSSQEFKKAFQNVLRIQCLRRKQ-SSKHA 355
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Publication No. US20050266522A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                Sequence 582, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 10
LENGTH: 353
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Best Local Similarity 26.4%;
Matches 97; Conservative 7
APPLICANT: Meng, Dr. Xun
APPLICANT: Chan, John W.
APPLICANT: Chan, John W.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Chan, John W.
APPLICANT: Benkovic, Stephen J.
TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: EPTM-P05-001
CURRENT APPLICATION NUMBER: US/11/249,847
CURRENT FILING DATE: 2005-10-12
PRIOR APPLICATION NUMBER: 10/436,549
PRIOR APPLICATION NUMBER: 60/379,626
PRIOR APPLICATION NUMBER: 60/379,626
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PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 09/314,006
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 08/467,559
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 10
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TITLE OF INVENTION: Human Amine Receptor
FILE REFERENCE: PF188D1C2
                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Frank D.
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CURRENT FILING DATE: 2004-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 RKAFLKI 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 VAVWVLAFLVNGFMIL-VSESWKDEGSECEPGFFSEWYILAITSFLEFVIPVILVAYFNM 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 VGEWKFSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 LFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYRTQHTGVLKIVTLM 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRR-----KSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRARRLAKSL 305
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o. US20060035270A1
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Pred. No. 6.1e-26;
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US-10-499-210-2
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; ORGANISM: Homo sapiens
US-11-249-847-582
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                  Sequence 2, Application US/10499210
Publication No. US20060052435A1
GENERAL INFORMATION:
APPLICANT: Pfizer Limited and Pfizer,
TITLE OF INVENTION: Compounds for the
TITLE OF INVENTION: Dysfunction
FILE REFERENCE: PC22046A
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Best Local
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SEQ ID NO 582
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CURRENT APPLICATION NUMBER: US/10/499,210
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APPLICATION NUMBER: 60/393,137
PTITING DATE: 2002-07-01
PTITING DATE: 2002-07-01
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APPLICATION NUMBER: 60/393,233
FILING DATE: 2002-07-01
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APPLICATION NUMBER: 60/393,211
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FILING DATE: 2002-07-01
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APPLICATION NUMBER: 60/393,197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 VAVWVLAFLVNGPMI----LVSESWKDEGSECEPGFFSEWYILAITSFLEFVIPVILVAY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                        324 VNRSHGQLKTDEQGLNTHGASEISEDQMLGDSQSFSRTDSDTTTETAPGKGKLRSGSNTG
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                                                                                                                                                                                                                                                            CCNEHLHMFTI -- WLGYINSTLNPLIYPLCNENFKKTFKRILHIR 486
                                                                                                                                                                                                                                                                                                    ATGPKSVWYRIAFWLOWENSFVNPLLYPLCHKRFQKAFLKIFCIK 376
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                                                               Treatment
                                                                 of Sexual
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; ORGANISM: Homo sapiens
US-11-165-024-3
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US-11-165-024-3
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Publication No. US20050266527A1
GENERAL INFORMATION:
    Matches
                          Best
                                                                                                                                                             SEQ ID NO 3
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Best Local
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                                        Query Match
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 10/006,394
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 09/228,420
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 08/465,971
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
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TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
FILE REFERENCE: PF187D1C2
CURRENT APPLICATION NUMBER: US/11/165,024
CURRENT FILING DATE: 2005-06-24
                                                                                                                                                                             SOFTWARE: PatentIn version 3.3
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                                                                                                                       TYPE: PRT
                                                                                                                                     LENGTH:
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                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 FLVNGPMILVSESWKDEG--SECEPGFFSEWYILAITSFLEFVIPVILVAYFNMNIYWSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 CCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVALMITAVWVLA
                                                                                                                                         350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGVISIP--LYIPHTLFEWDFGKE
    99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSICODTALGGPGFQERGGELKREEKTRNSLSPTIAPKLSLEVRKLSNGRLSTSLKLGPL 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQRRRKRILTRQNSQCNSVRPGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAVSCPLLFGFNTTGDPTVCSISNPDFVI--YSSVVSFYLPFGVTVLVYA----RIYVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAVSYR--TQHTGVLKIVTLMVAVWVLA 143
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                      17.0%; Score 344; DB 7; 26.5%; Pred. No. 3.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.2%; Score 348.5; DB (
28.9%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB 0130219.9
74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PQTLSPD---PAHLELKRY 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
    131;
                                        Length 350;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
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      14;
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Search completed: March 28, 2006, 14:03:32 Job time: 25 secs